



Biological Sciences

A paradise for *Maldane sarsi antarctica*: preliminary characterization of the marine soft-bottom fauna of False Bay (Livingston Island, South Shetland Islands, Antarctica)

Miguel Bascur^{1,†}, Andrea Prófumo^{1,†}, Mariona Gonzalez-Pineda¹, Pere Monràs-Riera¹,
Tomás Azcárate-García^{1,2}, Àlex Aubach-Masip¹, Marina De Llobet^{1,3}, Guillem Molina-Vacas¹,
Yara Tibiriçá⁴, Elisenda Ballesté⁵, João Gil⁶ and Conxita Avila¹

¹Department of Evolutionary Biology, Ecology, Environmental Sciences, and Biodiversity Research Institute (IRBio), Faculty of Biology, Universitat de Barcelona, Barcelona, Catalonia, Spain; ²Department of Marine Biology and Oceanography, Institute of Marine Sciences (ICM-CSIC), Barcelona, Catalonia, Spain; ³School of Ocean Sciences, Bangor University, Menai Bridge, UK; ⁴University of Guam, Marine Laboratory, Mangilao, GU, USA; ⁵Department of Genetics, Microbiology and Statistics, Faculty of Biology, Universitat de Barcelona, Barcelona, Catalonia, Spain and ⁶Centre of Marine Sciences (CCMAR), University of Algarve, Campus de Gambelas, Faro, Portugal

Abstract

Soft-bottom areas are among the least explored ecosystems in Antarctica. To improve our understanding of these environments, we performed a preliminary assessment of the marine macrobenthic fauna in False Bay, Livingston Island, near Huntress Glacier (South Shetland Islands, Antarctica). Fourteen Van Veen grabs (0.018 m² area) were deployed at two stations within the bay at depths of 174–210 m. The samples provided values up to 159 556 individuals m⁻² within 15 major taxonomic groups. Annelida Polychaeta was predominant (~93%), followed by Ophiuroidea and Bivalvia at the external station and Bivalvia and Amphipoda at the internal site. Maldanid polychaetes, particularly *Maldane sarsi antarctica*, constituted 84.62–90.74% of the samples. Total biomass was 6673.25 grams of wet weight per square metre, mainly from Ascidiacea, Polychaeta, Holothuroidea and Ophiuroidea. Approximately 12% of the macrofauna inhabited the sediment (epifauna), while 88% lived into the sediments (infauna). Regarding feeding modes, specimens were detritivores (77.91–82.71%), suspension-feeders (7.59–13.37%) and, infrequently, predators (4.07–5.07%) and grazers (4.63–4.65%). According to the compilation of occurrence records in the Southern Ocean, *M. sarsi antarctica* has a circum-Antarctic distribution. Furthermore, the population of this species in False Bay appears to be stable and undisturbed with a normal distribution in size structure, with a higher proportion of individuals at intermediate sizes (2.85–4.26 cm). This study provides for the first time detailed descriptions of the macrofauna from the soft bottoms of False Bay, representing a preliminary effort to monitor ecological shifts in this critically important and understudied region, which is experiencing rapid environmental changes within Antarctic marine ecosystems.

Keywords: Annelida Polychaeta; marine invertebrates; polar assemblages; sedimentary habitats; Southern Ocean

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Introduction

Marine soft sediments are among the most widespread habitats in the world's oceans and play a fundamental role in the functioning of marine ecosystems (Gray 2002, Pan & Pratolongo 2022). These habitats are primarily composed of fine-grained sediments such as mud, sand and gravel and host many diverse benthic communities that are crucial in processes such as energy transfer in trophic networks, nutrient and carbon cycling, contaminant

removal and secondary production (Snelgrove *et al.* 1997, Lohrer & Hancock 2004, Schratzberger & Ingels 2018). Currently, marine soft sediments face many threats, including climate hazards and anthropogenic pressures (Brierley & Kingsford 2009, Gissi *et al.* 2021, Williamson & Guinder 2021). For instance, ocean warming and pollution can alter sediment characteristics, leading to shifts in species compositions and ecosystem services (Altafim *et al.* 2023, Vlaminck *et al.* 2023). Despite their significance, marine soft sediments are still poorly studied, particularly in polar areas, making it crucial to obtain a deeper understanding of these ecosystems given the current global climate trends.

The composition of faunal assemblages inhabiting soft-bottom ecosystems is shaped by a complex interplay of environmental factors, where depth, sediment type and organic matter content are particularly relevant (Snelgrove 1999, Vause *et al.* 2019). Among the invertebrate macrofauna, the most representative phyla in these assemblages are annelid polychaetes, crustaceans, molluscs and echinoderms, although other annelids (e.g. echiurans and

Corresponding author: Miguel Bascur and Andrea Prófumo; Emails: mbas-cuba7@alumni.ub.edu; aprofumo@ub.edu

[†]These authors have contributed equally to this work

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sipunculans) and nemerteans are also present in lower abundances (Snelgrove 1998, Ellingsen 2001). The organisms living in these assemblages are typically characterized by limited mobility, and they may inhabit either into the sediment (infauna), the sediment surface (epifauna) or both (e.g. Pearson 2001). Regarding feeding strategies, suspension-feeders (both active and passive), deposit-feeders (surface or subsurface) and predators usually dominate these marine sediments, although other feeding types may also be present (Snelgrove 1999, Macdonald *et al.* 2012). Additionally, due to their three-dimensional body structures extending above the sediment, some of these organisms may act as ecosystem engineers and provide substrates for other organisms to attach to and grow upon (Rabaut *et al.* 2007, Meadows *et al.* 2012).

In the Southern Ocean, faunal assemblages differ from those found elsewhere in the world due to several environmental characteristics, such as isolation, water temperature and continental shelf depth (Barnes & Clarke 2011). Although all phyla can be found in this ocean, two types of soft-bottom assemblages can be differentiated: 1) those dominated by sessile suspension-feeding epifauna, such as sponges or ascidians, and 2) those dominated by infauna and mobile epifauna, such as polychaetes, bivalves and echinoderms (Gutt 2007 and references therein). Furthermore, because durophagy is absent in these environments, the main predators are species such as sea stars and nemerteans, among other vagile taxa (Dayton *et al.* 1975, Aronson & Blake 2001, Clarke *et al.* 2004, Ortiz *et al.* 2017).

Widely reported regional changes, such as the reduction of the annual duration of sea ice, the melting and retreat of marine-terminating glaciers and the collapse of ice shelves around Antarctica during recent decades, are significant threats to biodiversity in these zones (Gutt *et al.* 2011, Ducklow *et al.* 2013, Cook *et al.* 2016, Henley *et al.* 2019, Post *et al.* 2019, IPCC 2023). Considering that many of these Antarctic areas remain underexplored, predictions for the future of their soft-bottom marine biodiversity in the face of climate change are uncertain (e.g. Vause *et al.* 2019). This is especially true in the South Shetland Islands, an archipelago close to the Polar Front, a crucial boundary where cold Antarctic waters meet warmer sub-Antarctic waters (e.g. Orsi *et al.* 1995).

Annelid polychaetes represent one of the most common and abundant taxa in marine benthic communities worldwide, particularly in sedimentary environments (Knox 1977, Hutchings 1998, Crespo & Pardal 2020, Giangrande *et al.* 2020). Several studies have demonstrated their dominance in terms of species richness, abundance and biomass in soft-bottom habitats (Knox 1977, Hutchings *et al.* 1993, Smith 2000). This dominance is particularly notable in polar areas (Kendall *et al.* 2003, Piepenburg 2005, Clarke & Crame 2010, Pabis *et al.* 2011), where they may reach more than half of the total benthic invertebrate biomass (Knox 1977). Polychaetes play a critical role in ecosystems by creating new habitats and modifying the redox conditions of the sediment through bioturbation (Bolam & Fernandes 2002, Mermillod-Blondin 2011, Kristensen *et al.* 2012, Jumars *et al.* 2015). These processes are essential to allowing oxygenation and the transportation of surface materials to the deeper sediment layers, maintaining and even creating soft-bottom ecosystem structures.

Thus, to enhance our understanding of Antarctic marine soft-bottom assemblages in underexplored ecosystems threatened by global warming, this study aimed to provide a preliminary description of the marine fauna inhabiting False Bay in Livingston Island (South Shetland Islands). These new insights represent a valuable baseline for future studies assessing the broader ecological implications beyond the climate-induced changes in Antarctic ecosystems.

Methods

Study location

The present study was carried out during January 2023 (summer) at False Bay, Livingston Island (South Shetland Islands, Antarctica) in the framework of the CHALLENGE Antarctic campaign by our research group (Universitat de Barcelona). This cove of 6.4 km in length lies between Barnard Point and Hurd Peninsula, on the south side of Livingston Island (62°43'S, 60°22'W; Fig. 1). Within this bay, we selected two different stations to obtain a preliminary description of the marine benthic macrofauna: an exterior site and a more internal one (Fig. 1). These two stations were chosen based on their contrasting distance from Huntress Glacier, located in the innermost part of the bay, and according to the logistical necessities of our cruise. False Bay has some marine-terminating glaciers, with Huntress Glacier being the largest, despite having shown a gradual retreat in recent years (Cook *et al.* 2021).

Environmental variables

Oceanographic data, including seawater temperature (°C), salinity (PSU), chlorophyll-*a* (mg m⁻³) and dissolved oxygen (mg l⁻¹), were obtained from both stations within the bay using a Sea-bird SBE 11plus CTD (conductivity-temperature-depth) device to characterize the environmental conditions from the collection sites. The 10 deepest data points from each vertical profile, and thus closest to the biological sampling location, were pooled to obtain the mean and standard deviation for each station and variable (Table 1). Substrate descriptions rely on visual observations, indicating a detritic mud environment.

Sample collection and classification

More than 20 Van Veen dredges (0.15 × 0.12 × 0.40 m; 0.018 m² area) were deployed from the starboard side of the vessel, with a depth range of 174–210 m. Only some of these dredges retrieved sediments: 10 from the external station and 4 from the more internal station, thus rendering a total of 14 samples. All of the dredges' contents underwent meticulous sieving using seawater through a 1 mm mesh sieve. The organisms and sediment captured were subsequently relocated to the wet laboratory. Separation using tweezers was carefully performed to sort all of the macrofauna from the fine sediment. All of the specimens found were then categorized into broad taxonomic groups, mainly classes (although for crustaceans we used orders), and carefully preserved in pre-labelled bottles containing absolute ethanol. Later, at the laboratories of the Universitat de Barcelona, all individuals were counted, their wet weight was obtained and they were photographed using an Euromex® stereomicroscope. Finally, abundances and biomass data were standardized as individuals per square metre (ind. m⁻²) and grams of wet weight (WW) per square metre (g WW m⁻²), respectively. As we could not obtain sufficient replicates from the internal station and dredge samples were pooled at each site, a statistical comparison between both stations was not performed, although we provide here all of the descriptive data regarding the fauna collected.

Taxonomic identification and feeding guilds

Most specimens were preliminarily identified by the authors to the lowest possible taxonomic level using the available literature (Brueggeman 1998, Engl 2012, Rauschert *et al.* 2015, Xavier *et al.* 2020, Drennan *et al.* 2021). Then, the preliminary

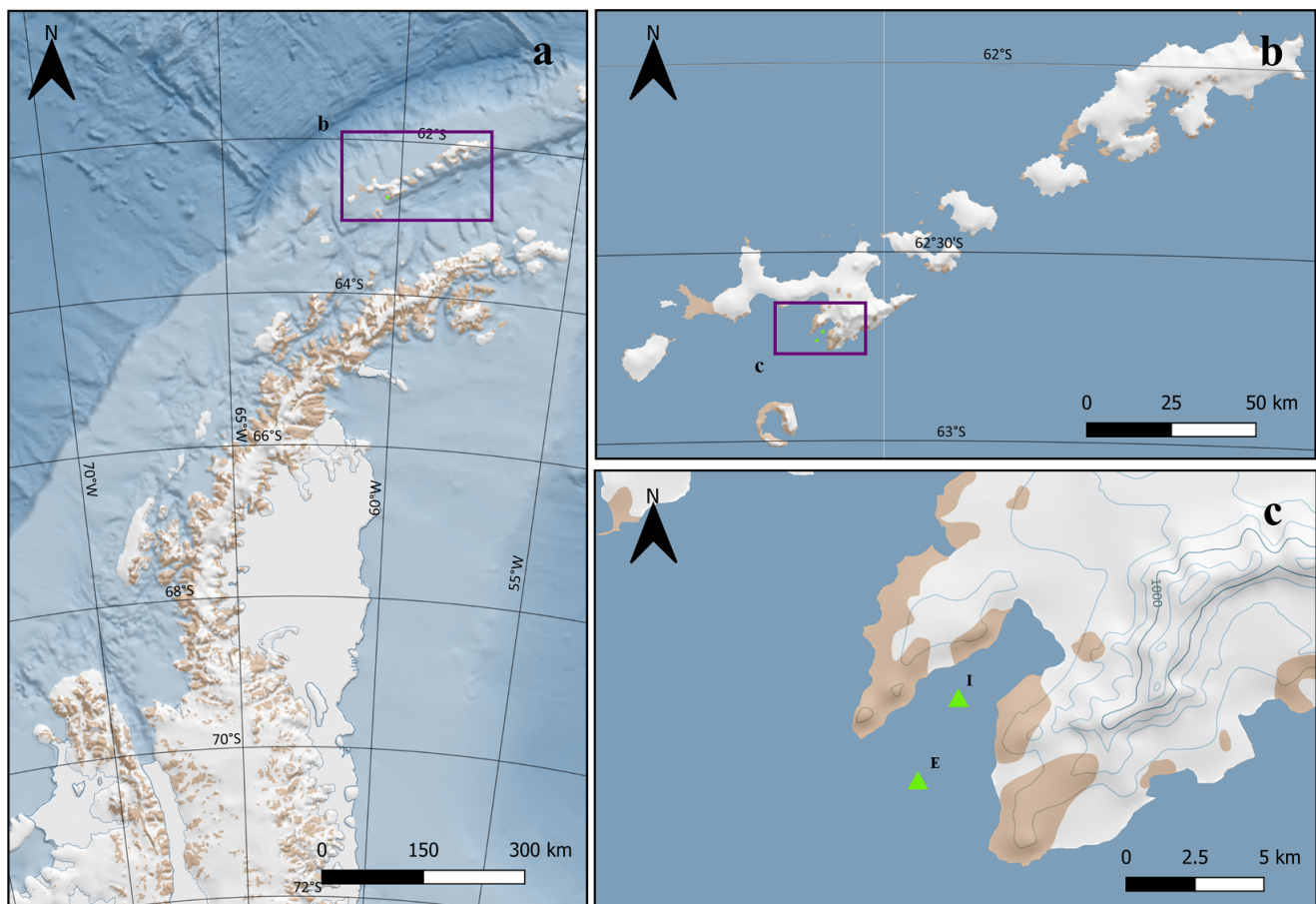


Figure 1. Sampling locations in a. the West Antarctic Peninsula and the South Shetland Islands, b. Livingston Island and c. within False Bay. Sampling locations are shown as green triangles (E = external station; I = internal station).

Table 1. Sampling location and characteristics of the stations, including dredge and CTD (conductivity-temperature-depth) device sampling coordinates, depths and environmental data. Data for environmental parameters indicate means \pm standard deviation.

Station	Latitude	Longitude	Dredge depth (m)	CTD depth (m)	Bottom type	Temperature ($^{\circ}$ C)	Chl- <i>a</i> (mg m^{-3})	Salinity (PSU)	DO (mg l^{-1})
Internal	62 $^{\circ}$ 42'30.71"S	60 $^{\circ}$ 21'48.65"W	174 \pm 4.60	150.00 \pm 0.03	Mud and gravel	1.75 \pm 0.01	0.18 \pm 0.01	34.14 \pm 0.01	6.82 \pm 0.01
External	62 $^{\circ}$ 43'53.70"S	60 $^{\circ}$ 23'41.84"W	209.77 \pm 4.23	185.25 \pm 0.03	Mud and gravel	0.82 \pm 0.01	0.08 \pm 0.01	34.34 \pm 0.01	5.99 \pm 0.01

Chl-*a* = chlorophyll-*a*; DO = dissolved oxygen.

identifications, together with their respective photographs, were sent to specialists of the different taxonomic groups to confirm their identification (Tables II & S1). Additionally, all organisms found were classified, based on the abundance data, using relative frequency according to their feeding behaviour (grazers, suspension-feeders, predators and detritivores) or their physical habitat (infauna or epifauna), following the most relevant literature (Jumars *et al.* 2015, Barnes & Sands 2017, Mohd Nasir *et al.* 2024, Souster *et al.* 2024). The detritivore functional group also included deposit-feeder specimens. Only for specimens that could alternate between both physical habitats (epifauna and infauna) or could present different feeding types, a frequency > 1 was recorded.

Distribution and population features of *Maldane sarsi antarctica*

Due to the clear dominance of *M. sarsi antarctica* Arwidsson, 1911 in the soft-bottom environment at our study sites, an

in-depth analysis of some of the ecological characteristics of this species was carried out. A comprehensive search of the spatial distribution of this species across the Antarctic region was conducted to provide context for its occurrence in False Bay. A preliminary search was conducted of georeferenced occurrence records compiled from the published literature (Siciński 1986, Ahn & Kang 1991, Cantone 1995, Parapar *et al.* 2011, Pabis & Siciński 2012) and public databases such as SCAR-MarBin (<https://www.vliz.be/projects/scarmarbin/>), OBIS (<https://www.obis.org/>), GBIF (<http://www.gbif.org/>) and Biodiversity.aq (<https://www.biodiversity.aq/>), selecting only those records that provided geographical coordinates. Occurrence records were obtained from Biodiversity.aq, given that this repository integrates data from all other relevant databases. Moreover, occurrence records were also extracted from research articles in which this polychaete species was recorded (see Data S1). The dataset was processed and visualised using QGIS v.3.40 software to generate a map representing its known distribution and

Table II. Summary of abundances and biomasses for the main groups and species found in this study. Data extracted from the full Table S1.

Taxa	External			Internal		
	Total ind. (n)	Abundance (ind. m ⁻²)	Biomass (g WW m ⁻²)	Total ind. (n)	Abundance (ind. m ⁻²)	Biomass (g WW m ⁻²)
Polychaeta	2538	141 000	1878	130	7222	71
<i>Maldane sarsi antarctica</i>	2302	127 888	1348.02	110	6111	56.08
Ophiuroidea	61	3389	889.17	-	-	-
Bivalvia	45	2500	38.11	4	222	2.51
Amphipoda	25	1389	18.25	3	167	2.15
Pycnogonida	20	1111	77.24	1	56	64.72
Bryozoa (Gymnolaemata)	14	778	213.07	-	-	-
Asciacea	8	444	1721.51	1	56	290.35
Isopoda	5	278	57.06	1	56	290.35

ind. = individuals; WW = wet weight.

also to display the sampling depths of each record in order to offer further insights into the species' bathymetric range. However, some studies reporting the presence of this species were not included in the dataset (e.g. Garraffoni *et al.* 2012), as they did not provide exact geographical coordinates or sampling depths nor specify its occurrence at a precise sampling station, despite confirming its presence in the study areas. In general, these studies do not refer to new distribution sites but rather to already-sampled locations that are represented in the compiled dataset (Data S1).

The size structure of the *M. sarsi antarctica* population in False Bay was also studied. To obtain a representative sample of the population, we used stratified sampling (Andrew & Mapstone 1987). The total population of 2412 individuals were divided into three strata based on body size, categorized as small, medium and large, as determined by visual observation. Once the population was stratified, the number of individuals in each stratum was counted. Each stratum was then assigned a sample size proportional to its representation in the total population using the calculation in Equation 1:

$$n_i = \frac{N_i}{N_{total}} \times n_{sample} \quad (1)$$

where n_i is the theoretical number of individuals from the stratum, N_i is the total number of individuals in stratum i , N_{total} is the total number of individuals in the population and n_{sample} is the subsample selected from the total population. Once the sample proportion for each stratum was determined as small (26.83%), medium (56.10%) or large (17.07%), 410 individuals (~17% of the total population) were randomly selected within each stratum to measure their total length. Using a Vernier calliper, the total length (from the tip of the head to the end of the pygidium) was then measured (in cm). Using the size database, the data were sorted in increasing order to determine the minimum and maximum size so as to obtain the total rank ($R = \text{maximum} - \text{minimum}$). Then, the interquartile range (IQR) was calculated by subtracting the size value of the first quartile (Q1) from the data of the third quartile (Q3). Using the IQR and the number of samples, the width of each interval was calculated using the Freedman-Diaconis rule (Freedman & Diaconis 1981), shown in Equation 2:

$$h = 2 \times IQR \times n^{-1/3} \quad (2)$$

where h is the width of each interval and n is the number of observations. Finally, the total rank (R) was divided by the interval width (h) to establish nine different and appropriate categories for the frequency histogram in order to display the population characteristics of the species' size.

Results

Environmental variables

The collected data from both stations in False Bay showed variations in the environmental conditions between the two sites (Table 1). The internal station, situated at a shallower depth, presented slightly warmer temperatures ($1.75 \pm 0.01^\circ\text{C}$ vs $0.82 \pm 0.01^\circ\text{C}$) and higher chlorophyll-*a* concentrations (0.18 ± 0.01 vs $0.08 \pm 0.01 \text{ mg m}^{-3}$) than the external site, located at a greater depth. Furthermore, the dissolved oxygen concentration was higher at the internal station ($6.82 \pm 0.01 \text{ mg l}^{-1}$) compared to the external one ($5.99 \pm 0.01 \text{ mg l}^{-1}$). Both stations shared similar sediment characteristics when visually evaluated, consisting of mud and gravel, indicative of a low-energy depositional environment.

Assemblage characteristics

A total of 159 556 ind. m⁻² were identified in this study, classified into 15 major taxonomic groups: Polychaeta, Bivalvia, Amphipoda, Ophiuroidea, Asteroidea, Pycnogonida, Isopoda, Holothuroidea, Asciacea, Priapulida, Nemertea, Cnidaria, Bryozoa, Gastropoda and Porifera (Fig. 2 & Tables II & S1). From these, total abundances were 151 778 ind. m⁻² at the external station and 7778 ind. m⁻² at the internal station, corresponding to 15 and 6 major taxonomic groups, respectively (Tables II & S1). For both stations, Polychaeta was the most abundant taxon (~93%; Fig. 3). Ophiuroidea (2.23%) and Bivalvia (1.65%) were the next more abundant taxa for the external station, while Bivalvia (2.86%) and Amphipoda (2.14%) were the next more abundant taxa for the internal one (Fig. 3).

The total biomass measured was 6673.25 g WW m⁻², of which 6239.25 g WW m⁻² corresponded to the external station and 434 g WW m⁻² corresponded to the internal station (Table S1). Asciacea (27.59%) and Polychaeta (30.10%) had similar percentages, followed by Holothuroidea (20.62%) and Ophiuroidea

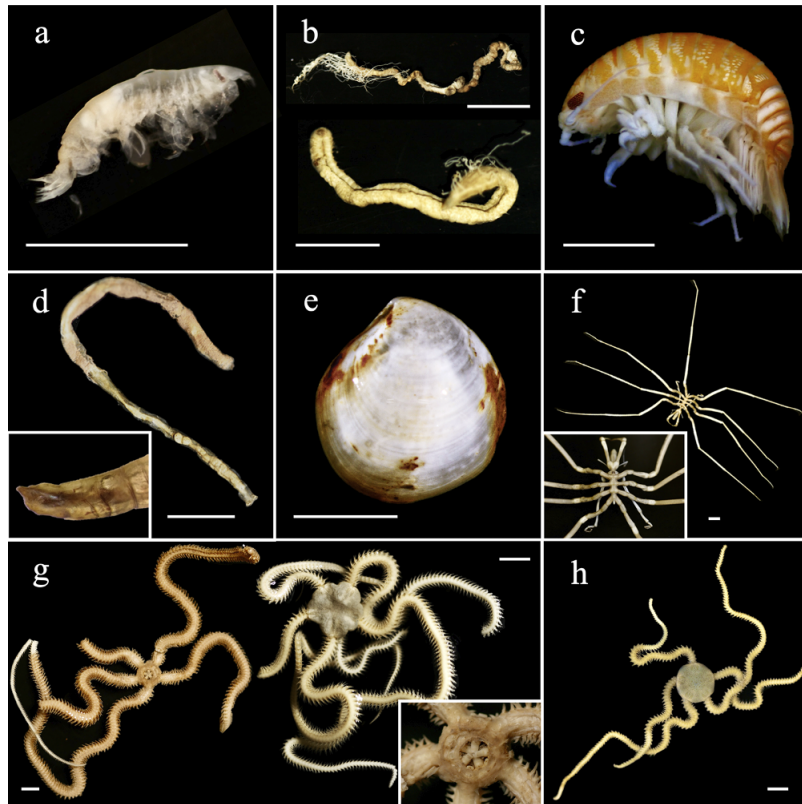


Figure 2. Images of the most representative specimens collected during the second expedition of the CHALLENGE project in False Bay (Livingston Island): **a.** Phoxocephalidae (Amphipoda), **b.** *Aphelocheata* sp. (Polychaeta), **c.** *Natatolana* sp. (Isopoda), **d.** *Maldane sarsi antarctica* (Polychaeta), **e.** *Thyasira debilis* (Bivalvia), **f.** *Nymphon charcoti* (Pycnogonida), **g.** *Amphiura* cf. *joubini* (Ophiuroidea) and **h.** *Amphiura* sp. (Ophiuroidea). All scale bars = 1 cm, except for **e.** scale bar = 2 mm.

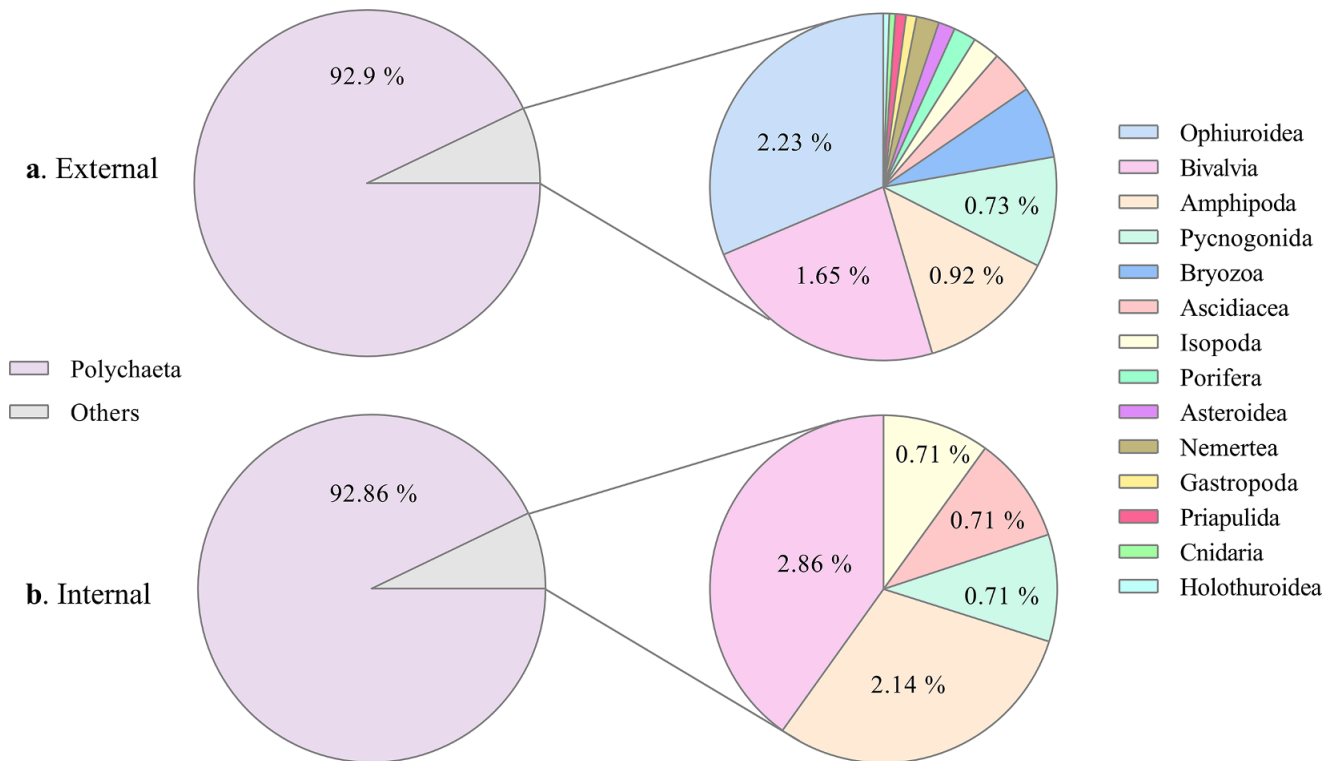


Figure 3. Contribution to relative abundances of taxonomic groups found at the **a.** external and **b.** internal stations. The pie charts show the overall composition of assemblages, including polychaetes, with the expanded sections detailing the distribution of other taxa.

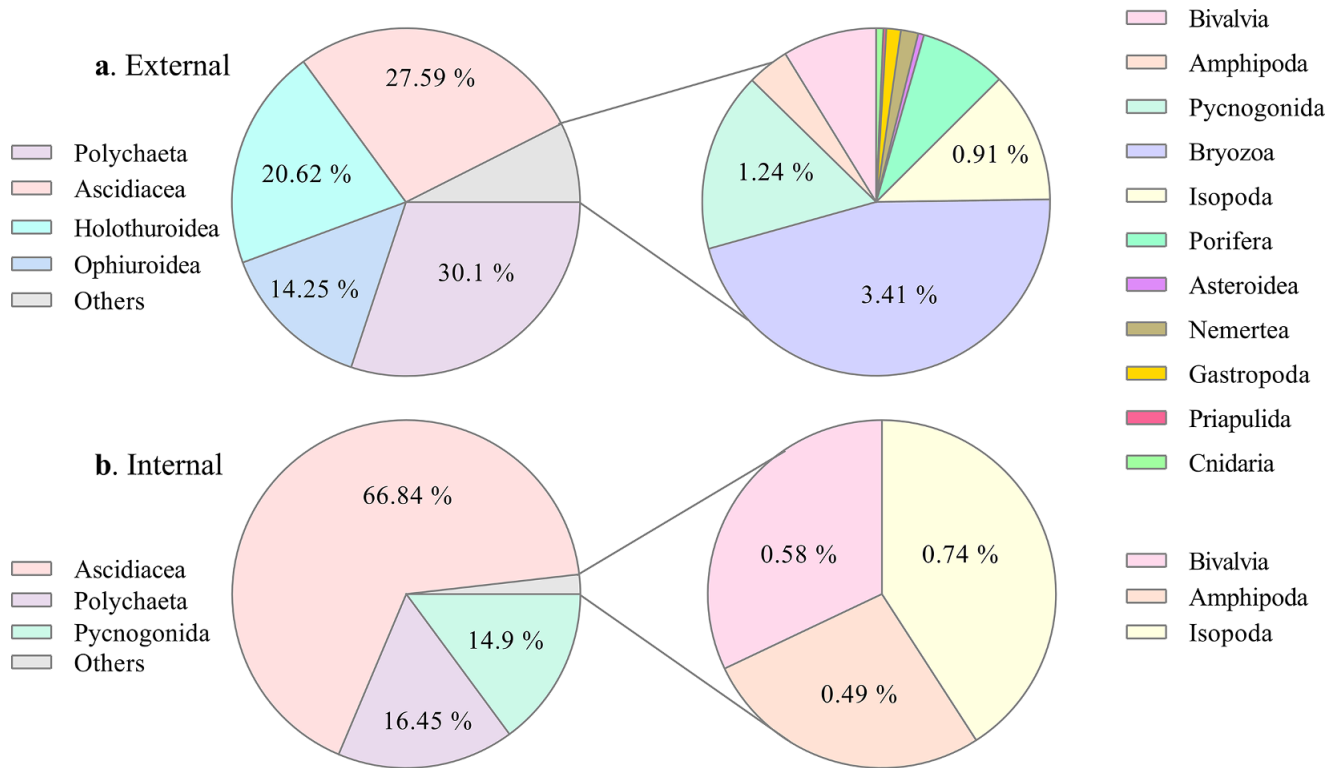


Figure 4. Contribution to relative biomasses of taxonomic groups found at the **a.** external and **b.** internal stations. The pie charts show the overall composition of assemblages, with the expanded sections detailing the distribution of other taxa.

(14.25%), in terms of being the main contributors to the biomass at the external station (Fig. 4). At the internal station, the biomass was instead dominated by Ascidiacea (66.84%), followed by Polychaeta (16.45%) and Pycnogonida (14.90%; Fig. 4).

Regarding Polychaeta, both sampling stations exhibited a high relative abundance, ranging from 84.62% to 90.74% for the family Maldanidae (i.e. *M. sarsi antarctica*; Fig. 5 & Table II), with a biomass of 1348.02 g WW m⁻² at the external station and 56.08 g WW m⁻² at the internal station (Fig. 6 & Tables II & S1). After maldanids, Cirratulidae (3.94–9.23%), Lumbrineridae (1.65–2.31%) and Spionidae (0.87–1.54%) were the most abundant polychaete families at both stations. For polychaetes, the main difference between the stations was the total number of families, with 15 being present at the external station compared to 7 being present at the internal station (Table S1).

The distributions of functional groups based on their feeding behaviour (grazers, suspension-feeders, predators and detritivores) were similar at both stations, with a predominant contribution of detritivores. However, the external station showed slightly higher proportions of predators (5.07%) and detritivores (82.71%) but a lower proportion of suspension-feeders (7.59%) compared to the internal station (4.07%, 77.91% and 13.37%, respectively; Fig. 7). The contributions of the infauna and the epifauna were also similar at both stations, with much higher values observed for the infauna than the epifauna (Fig. 7).

Distribution and population features of *Maldane sarsi antarctica*

A total of 186 previous records were found for *M. sarsi antarctica*, in a depth range from 40 to 3700 m. Our map indicates a

circum-Antarctic distribution for this species in the Antarctic benthos, with a major sampling focus on the South Shetland Islands and the Bellingshausen Sea and a significant lack of records in the southern Indian Ocean (Fig. S1 & Data S1).

The size distribution of *M. sarsi antarctica* ranged from 0.73 to 7.78 cm, with the highest concentration of individuals in the 2.85–3.55 cm (21.95%) and 3.55–4.26 cm (20.73%) intervals (Fig. S2, Table S2 & Data S2). The distribution follows a unimodal pattern, with a greater abundance of organisms in intermediate size classes and a gradual decrease towards the extremes (Fig. S2, Table S2 & Data S2). Therefore, these results indicate that the population is dominated by individuals in intermediate developmental stages, with fewer very small or large organisms.

Discussion

This study provides a first local-scale characterization of the marine soft-bottom assemblages inhabiting False Bay (Livingston Island). Our results show that benthic assemblages were dominated by Polychaeta in terms of relative abundance and a shared dominance of Ascidiacea, Ophiuroidea and Pycnogonida in terms of relative biomass, suggesting their successful adaptation to efficiently exploit the resources of this habitat. In particular, False Bay is a paradise for the maldanid *M. sarsi antarctica*, which is the most abundant species by far. Considering that several physical and ecological changes have been recorded widely in Antarctica due to global change and anthropogenic causes (Cook *et al.* 2016, Rogers *et al.* 2020), this study represents a first step towards providing a baseline for future studies addressing marine conservation policies and the effects of these changes on these particular soft-bottom marine ecosystems.

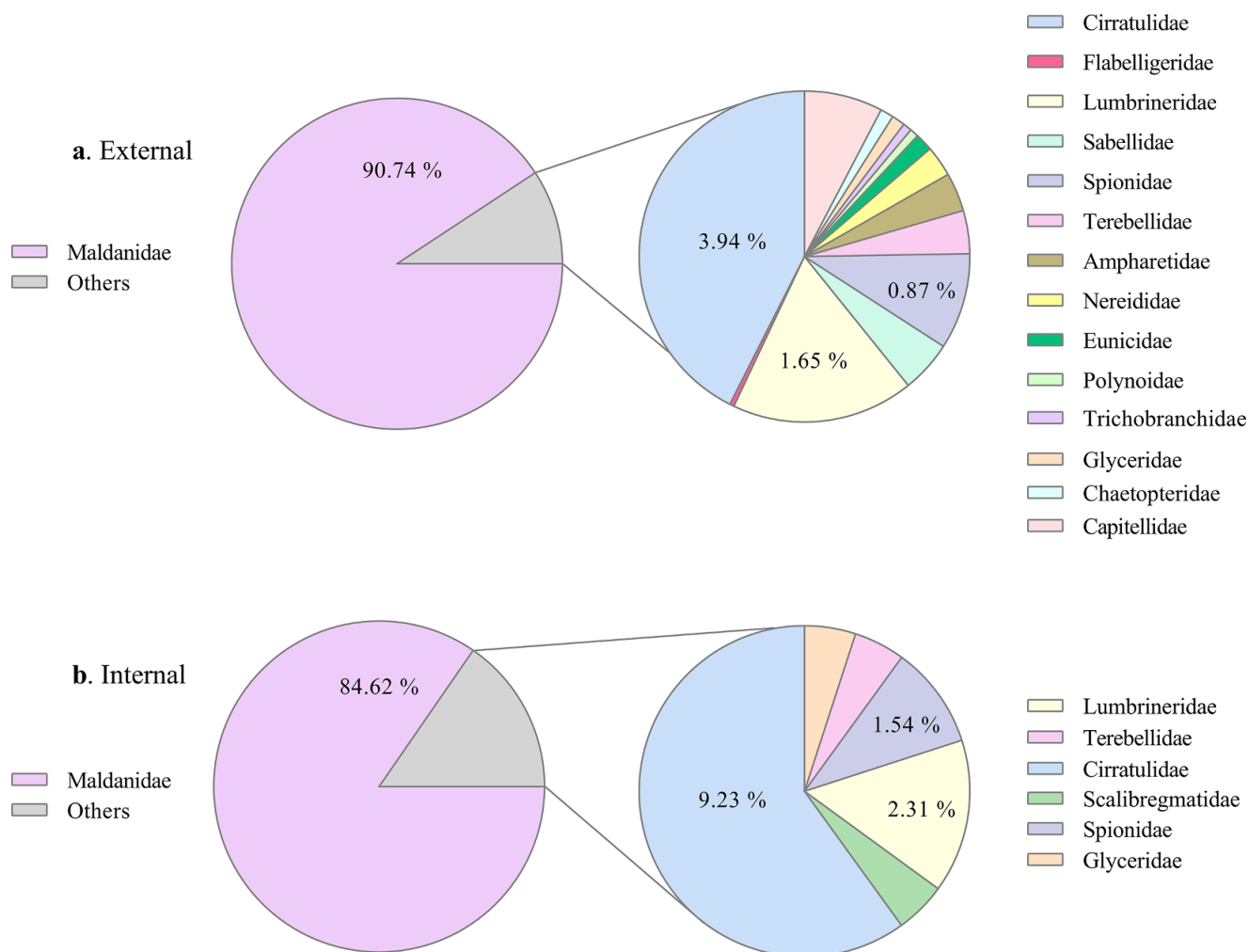


Figure 5. Contribution to relative abundances of different Polychaeta families found at the **a.** external and **b.** internal stations. The pie charts show the overall composition of assemblages, including Maldanidae, with the expanded sections detailing the distribution of other families.

Composition of benthic assemblages

Studies on soft-bottom benthic macrofauna involving both infaunal and epifaunal sources are relatively scarce, especially for Antarctica (Table III; Jażdżeski *et al.* 1986, Sáiz-Salinas *et al.* 1997, Arnaud *et al.* 1998, Angulo-Preckler *et al.* 2017b, 2018). Additional studies are required to determine the current situation and the effects of global change in polar areas, including with regard to glacier retreat. Most recent studies, however, focus mainly on assessing changes in the mega-epifauna around Antarctica through seafloor imagery and on infaunal descriptions using environmental DNA (e.g. Vause *et al.* 2019, Grimes *et al.* 2023). Our results reveal that in False Bay the dominant group was Polychaeta, followed by lower abundances of Bivalvia, Amphipoda and Ophiuroidea (only at the external station). The observed dominant taxonomic groups in this study align with previous descriptions from other regions of the planet (Table III). In such reports, with some exceptions, the Annelida, Crustacea, Mollusca and, sometimes, Echinodermata (especially in Antarctica) are the most dominant groups, even though differences exist in the sedimentary environment, the depth sampled (~5–4700 m) or the collecting methods used (e.g. Agassiz trawls, Van Veen dredges, box corers, scuba diving; Table III). These study areas include the tropical deep sea (Cosson *et al.* 1997, Quintanar-Retama *et al.* 2023), temperate areas

(Sardá *et al.* 1995, Martins *et al.* 2013, Soto *et al.* 2017), Arctic zones (Ellingsen 2001, Ellingsen & Gray 2002) and the South Shetland Islands in Antarctica (Sáiz-Salinas *et al.* 1997, Arnaud *et al.* 1998, Angulo-Preckler *et al.* 2017a,b, 2018; Table III). However, in contrast to our work, in these previous studies there was no such clear dominance of a single group, and the total abundances were distributed among two or more different taxonomic groups. Only one previous study carried out in Admiralty Bay (King George Island, South Shetland Islands) found similar results to those reported here in terms of dominance, with Polychaeta constituting 67.7% of the total fauna at 250 m depth, and Bivalvia reaching 86% of the total fauna at 15 m depth (Jażdżeski *et al.* 1986). In our study, the substantial differences in abundances between the internal and external sites could be related to the low number of replicates obtained in the study, but it could also be related to the distinct environmental parameters reported, such as the slightly higher temperature, higher chlorophyll-*a* concentration and higher dissolved oxygen concentration at the internal site. The internal site, being closer to the glacier front, was probably colonized much later than the external one, and this is relevant for both the species composition and the biomass found. In addition, near-shore marine Antarctic biodiversity may also be affected by shifts in the ice sheet caused by climate change, altering essential

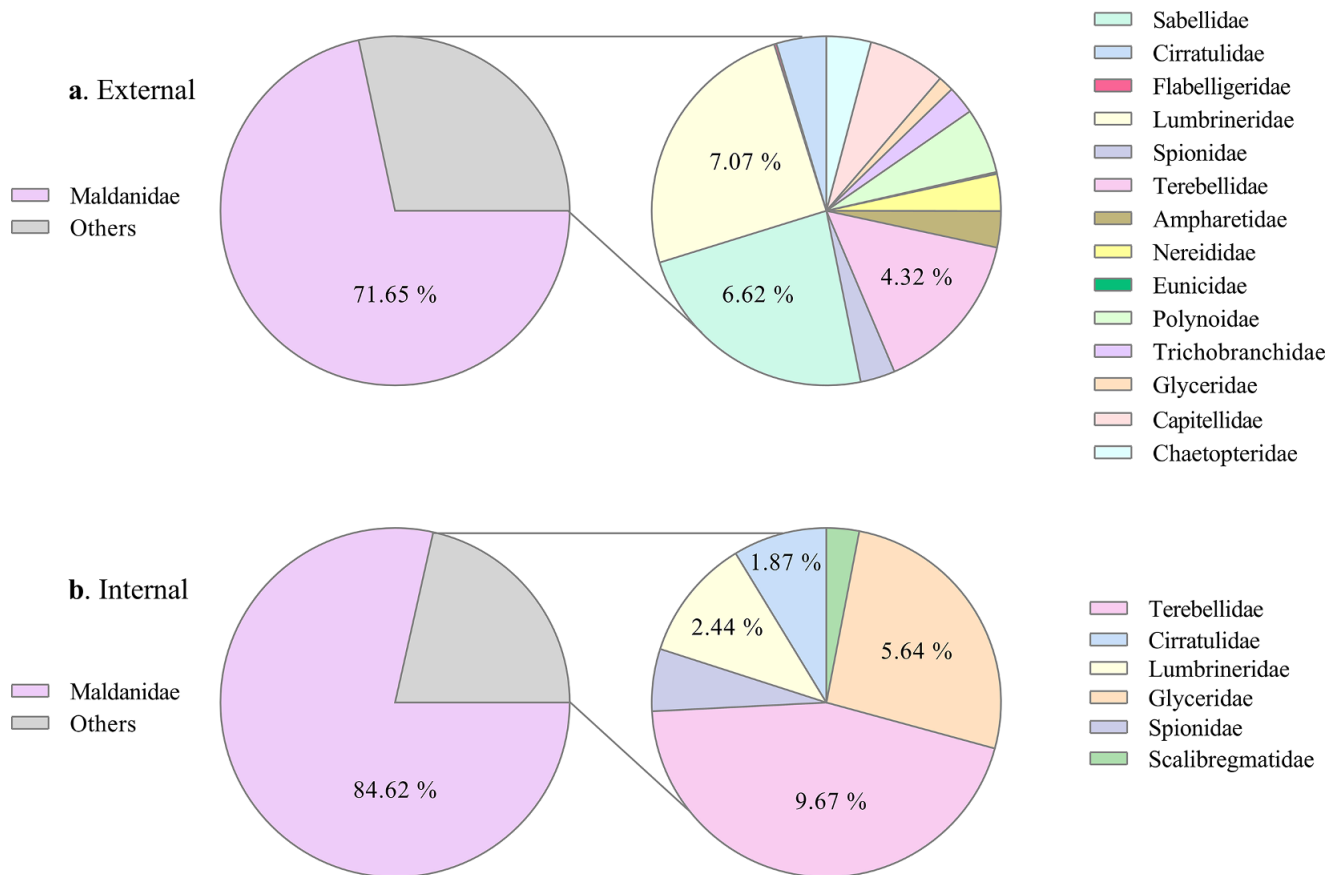


Figure 6. Contribution to relative biomasses of different Polychaeta families found at the **a.** external and **b.** internal stations. The pie charts show the overall composition of assemblages, with the expanded sections detailing the distribution of other taxa.

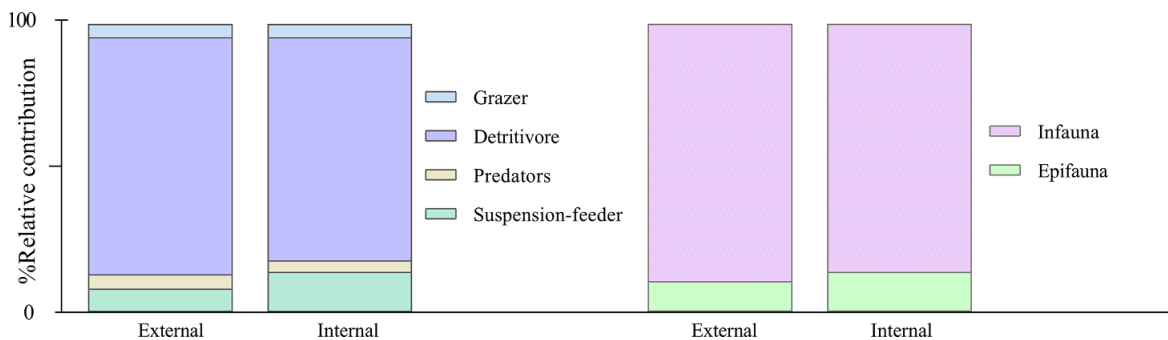


Figure 7. Relative contribution (%) of all sampled individuals according to their feeding behaviour (left) and physical habitat (right).

habitats (Pritchard *et al.* 2012, Noble *et al.* 2020). For instance, ocean warming has accelerated the melting of glaciers and the collapse of several ice shelves (Cook *et al.* 2016, Davison *et al.* 2023). Additionally, sea ice now forms later and melts earlier within a calendar year, contributing to the intensification of global warming (e.g. Purich & Doddridge 2023). Further studies are needed to carefully consider both of these possibilities.

Biomass in False Bay, however, was not dominated by a particular taxon but showed a distribution between Ascidiacea, Polychaeta, Holothuroidea, Ophiuroidea and Pycnogonida. These data are similar to those obtained in previous Antarctic studies, where biomass was also distributed among different groups, such as Ascidiacea, Echinodermata, Porifera, Polychaeta and, occasionally, Bryozoa (Jażdżeski *et al.* 1986, Sáiz-Salinas *et al.* 1997, Arnaud *et al.*

1998). Considering the patchiness of Antarctic marine assemblages at small spatial scales and the complexity of the environmental variations, it is usually assumed that assemblage compositions can be highly variable (Gutt 2007, Gutt *et al.* 2019). According to assembly theory, both stochastic and deterministic factors shape the structure of these marine communities (Vellend 2016). It is well established that marine fauna possessing specialized traits to exploit specific microhabitats can successfully colonize these areas, forming assemblages based on habitat affinity (Sebens 1991, Convey *et al.* 2014). Unfortunately, few studies have addressed these dynamics in Antarctica, rendering the current conclusions only preliminary. Some research suggests that, at large spatial scales, certain assemblages are primarily influenced by random processes (e.g. Valdivia *et al.* 2021), whereas studies at smaller

Table III. Main taxonomic groups, based on the total abundance, found in previous similar studies from soft-bottom habitats around the world, from low to high latitudes.

Dominant groups	Depth (m)	Total abundance (ind. m ⁻²)	Geographical area	Reference(s)
Polychaeta, Nematoda, Tanaidacea, Isopoda/Amphipoda, Bivalvia	185–4600	231.5–5403; 113–1388	Tropical deep sea	Cosson <i>et al.</i> (1997), Quintanar-Retama <i>et al.</i> (2023)
Polychaeta, Bivalvia, Nematoda, Nemertea/Ophiuroidea, Amphipoda	8–195	70–13 070 ^a ; 1416–3440; 398–73 250	Temperate	Sardá <i>et al.</i> (1995), Martins <i>et al.</i> (2013), Soto <i>et al.</i> (2017)
Polychaeta, Crustacea, Mollusca, Echinodermata	65–434	902–1848 ^a ; 20 804–101 992 ^a	Arctic	Ellingsen (2001), Ellingsen & Gray (2002)
Polychaeta, Bivalvia, Ascidiacea Ophiuroidea, Amphipoda	40–850	160–4380	Livingston Island and western Antarctic Peninsula	Sáiz-Salinas <i>et al.</i> (1997), Arnaud <i>et al.</i> (1998) ^b
Bivalvia, Polychaeta, Amphipoda	15–250	889–36 213	King George Island, Antarctica	Jażdżeski <i>et al.</i> (1986)
Polychaeta, Oligochaeta, Nematoda, Echinodermata Mollusca, Amphipoda	5–25	2578–205 625	Deception Island, Antarctica	Angulo-Preckler <i>et al.</i> (2017b, 2018) ^b
Polychaeta, Ophiuroidea, Bivalvia, Amphipoda	174–210	7778–151 778	False Bay, Livingston Island, Antarctica	This study

^a These values were calculated from the original data.

^b Abundance data not available.

ind. = individuals.

scales indicate that environmental filtering is the dominant driver (e.g. Valdivia *et al.* 2020). Thus, the spatial scale at which assemblage mechanisms are examined appears to be highly relevant. In this context, we propose that strong small-scale environmental filtering in False Bay has probably produced local assemblages characterized by highly convergent functional traits, such as those observed in terms of the dominance of deposit-feeders (Gutt 2007). This assemblage composition could be related to the unique characteristics of the available organic matter, sediment grain size or seafloor stability of this particular glacier bay (Sañé *et al.* 2012, Learman *et al.* 2016, Vause *et al.* 2019). Further studies are needed to clarify all of these relationships, and in particular why *M. sarsi antarctica* is 'in paradise' within False Bay, exhibiting the highest values for abundance and biomass of all of the taxonomic groups found there.

Benthic assemblages in False Bay are clearly dominated by deposit-feeding infauna, suggesting that sedimentation of organic matter from phytodetritus to the seabed plays a fundamental role in shaping the trophic structure of the ecosystem, providing a constant food source for these organisms (Gutt 2007, Angulo-Preckler *et al.* 2018). In this context, previous studies have proposed a 'food banks' theory for Antarctica (Glover *et al.* 2008, Mincks *et al.* 2008, Smith *et al.* 2012). This theory suggests that, due to the cold temperatures of the Southern Ocean, organic matter reaching the seafloor from phytodetritus flux and/or resuspension can remain available year-round for consumption by detritivorous (e.g. deposit-feeder) organisms (Glover *et al.* 2008). In contrast, the lower abundances of filter-feeding epifauna, such as Bryozoa and Ascidiacea, may indicate a more limited connection between the water column and the benthos, potentially resulting from the stability of the seabed, where the lack of strong currents reduces the availability of suspended particles for filter-feeders (Arnaud *et al.* 1998, Gutt 2007, Dunlop *et al.* 2020). Another potential cause of the low amount of epifauna in False Bay could be the dominant grain size of the sediment. Because of the lack of strong currents, the type of sediment that would accumulate most in this bay is detritic mud. As reported previously, epifaunal species are more

abundant in sediments with medium or large grain sizes, such as sand or gravel, than in muddy sediments (Gray 2002, Zhulay *et al.* 2019). However, despite the predominance of detritivores in False Bay, there were also some mobile epifaunal taxa characteristic of these infaunal-dominated assemblages that could obtain their food through predation or grazing, such as Ophiuroidea, Asteroidea, Amphipoda or Isopoda, although they appeared in much lower densities. This scenario suggests that the benthic community in this area may be highly specialized, with adaptations that enable organisms such as detritivores to thrive in an environment with specific environmental characteristics and ecological niches that support their development.

Ecological importance of Polychaeta and population features of *Maldane sarsi antarctica*

It has been widely described that polychaetes can significantly alter sediment conditions, which in turn can modify the structure and composition of benthic communities, emphasizing their role as engineering species in sedimentary marine ecosystems (Sanders *et al.* 1962, Levin *et al.* 1997, Waldbusser *et al.* 2004, Kongsrud & Rapp 2012). In our study, polychaetes accounted for ~93% of the total relative abundance obtained, with totals of 15 and 7 different families observed at the external and internal stations, respectively. Those results are within the values of previous studies examining soft-bottom polychaete assemblages in Antarctica, with numbers of families ranging from 13 to 27 (Parapar *et al.* 2011, Pabis & Sobczyk 2015, Paiva *et al.* 2015, Angulo-Preckler *et al.* 2017b). This contrasting composition may be associated with various factors such as depth, sediment grain size and organic matter content.

Remarkably, the family Maldanidae emerged as a key group in our study, representing 90.74% of the total abundance for the external station and 84.62% for the internal station. Maldanids are known for building tubes in soft and mixed sediments in both horizontal and vertical orientations (Day 1967, Jiménez-Cueto & Salazar-Vallejo 1997, De Assis *et al.* 2007). These tube constructions allow them to inhabit a wide range of habitats, from the

intertidal region to the deep sea (Paterson *et al.* 2009, De Assis & Christoffersen 2011). Maldanids feed mainly on organic matter, either in surface or in subsurface deposits, contributing to sediment irrigation and the supply of fresh organic matter for other infaunal organisms (Fauchald & Jumars 1979, Rouse & Pleijel 2001, Dufour *et al.* 2008, Jumars *et al.* 2015). Previous studies found that one of the most abundant maldanid species in Antarctica was *M. sarsi antarctica* Arwidsson, 1911, with maximum densities of between 139 and 2786 ind. m⁻² (e.g. San Martín *et al.* 2000, Siciński 2000, Siciński *et al.* 2011, Pabis & Sobczyk 2015, Cataldo-Mendez *et al.* 2024). This species was also the most dominant in our study, reaching up to a maximum abundance of 12 794 ind. m⁻² in False Bay. Our data showed much higher abundances of this polychaete species than in previous studies on soft bottoms around the South Shetland Islands at depths ranging from 46 to 694 m (e.g. Jażdżeski *et al.* 1986, Sáiz-Salinas *et al.* 1997). On the contrary, although the total polychaete assemblage is richer and more abundant at the shallower and volcanic-influenced habitat of Deception Island, this particular species is completely absent (Angulo-Preckler *et al.* 2017b, 2018). These findings suggest that the exceptionally high densities observed in False Bay reflect a combination of favourable food availability and stable benthic conditions that support deposit-feeding species while limiting the presence of suspension feeders. Additionally, recent research indicates that the energy content of this species is lower in areas near melting glaciers compared to more distant sites (Cataldo-Mendez *et al.* 2024). These findings collectively suggest that *M. sarsi antarctica* is a keystone species in Antarctic soft-bottom ecosystems, and further research on the species is essential for predicting how such marine assemblages might respond to global change.

Maldane sarsi antarctica has a circum-Antarctic distribution, probably influenced by oceanographic, ecological and evolutionary factors (Fig. S1). As a sedentary polychaete adapted to cold waters, its dispersal is driven by Antarctic marine currents that facilitate genetic connectivity and larval transport (Rogers 2007, Thatje 2012, Güller *et al.* 2020, Muñoz-Ramírez *et al.* 2020). Their trochophore larva, with its high dispersal potential, plays a key role in this process (De Assis *et al.* 2021). Furthermore, the abundance of soft-bottom habitats in Antarctica provides an ideal environment in which maldanids can build tubes, supporting their ecological success (Pan & Pratolongo 2022). Its wide distribution also suggests its persistence in glacial refugia, with evolutionary and plastic adaptations, such as cold and depth tolerance, enabling its survival through environmental changes (Thatje *et al.* 2005, Hoffmann & Sgrò 2011, Munday *et al.* 2013). These characteristics, combined with the fact that the size-frequency histogram of this population displays a normal distribution with a central peak, suggest a stable and undisturbed population with balanced recruitment and mortality rates (Fig. S2).

Limitations of the study and future perspectives

The present study was conducted at two stations within a specific Antarctic fjord based on a limited sampling scope that did not allow for statistically representative spatial comparisons to be made within the bay. Despite this clear limitation, our study offers a comprehensive biological and ecological characterization of marine assemblages in a relatively underexplored region, establishing an important baseline for future research. These preliminary findings are significant for understanding the structure and functioning of the ecosystem and may also be useful in the development of conservation strategies for this region. Further studies should analyse the

composition of the assemblages along the fjord after species begin to colonize the ice-free seabed following glacier retreat (Grange & Smith 2013, Sahade *et al.* 2015, Lager *et al.* 2017). It is important to note that although Huntress Glacier is not retreating as fast as other glaciers in the region (e.g. Cook *et al.* 2016), studying such changes is key. In addition, it would be interesting to relate these biological variables with environmental data (e.g. chlorophyll-*a*, sediment grain size, temperature) to obtain a more holistic view of this ecosystem. These kinds of studies are also useful for improving our understanding of how fjords are becoming pivotal 'blue carbon' ecosystems in terms of negative feedback for climate change by sequestering and storing organic carbon in new ice-free habitats (Barnes *et al.* 2020, Zwerschke *et al.* 2022).

Several limitations were encountered when searching for biological and ecological data regarding *M. sarsi antarctica* in the literature. First, data on abundances and specimen sizes were not always provided (most of the available records do not provide species-specific quantitative information). This is because abundance data for *M. sarsi antarctica* were mainly reported collectively, grouping this species with other, different species from benthic assemblages of Polychaeta, while specimen size data were often completely absent. This limitation highlights the need for more specific quantitative studies on Antarctic fauna. Second, although 186 records of *M. sarsi antarctica* were found across the Southern Ocean (Fig. S1 & Data S1), some previous studies have identified this species as the parent species *Maldane sarsi* Malmgren, 1865 (e.g. Drennan *et al.* 2021), without specifically mentioning the subspecies *M. sarsi antarctica*. This is probably due to the fact that the subspecies' diagnostic characteristics (colour and gland patterns) are not always considered robust taxonomic traits (Wang & Li 2016). Though recent studies, including Brasier *et al.* (2016), have suggested that the genetic differences and long geographical distances between Antarctic populations and the type locality of *M. sarsi* raise questions about the status of *M. sarsi antarctica* as a subspecies, being more likely a valid species on its own. Thus, although these records as *M. sarsi* were not considered in our analysis, they probably correspond to the same Antarctic subspecies here discussed. This issue highlights a gap in the current literature and in accurately identifying Antarctic *M. sarsi*, emphasizing the urgent need for further taxonomic clarification.

Conclusions

Our findings provide the first description of the benthic marine fauna from False Bay (Livingston Island, South Shetland Islands, Antarctica), revealing an assemblage dominated by infaunal, deposit-feeding polychaetes. In particular, False Bay is a paradise for the circum-Antarctic-distributed polychaete *M. sarsi antarctica*, which appears to have a stable and undisturbed population. Our data highlight the importance of exploring poorly studied areas to improve our knowledge of Antarctic biodiversity. Moreover, as many factors are currently threatening polar ecosystems, our results are key to establishing a baseline for assessing future changes in benthic assemblages, especially those related to global change and other human impacts.

Supplementary material. To view supplementary material for this article, please visit <http://doi.org/10.1017/S0954102025000185>.

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Competing interests. The authors declare none.

Author contributions. MB and CA conceptualized and designed the study; MB, AP, MG-P, PM-R, TA-G, AA-M, GM-V, YT, EB and CA were responsible for sample collection; MB, AP, MG-P, PM-R, TA-G, AA-M, MdL and JG conducted the laboratory analyses and bioinformatic analyses; MB and AP processed, interpreted and discussed the results; MG-P performed the data visualization; CA supervised the study and secured the funding; MB and AP drafted the initial manuscript with contributions from all of the authors to the final version.

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