



OPEN Benthic biodiversity in Collins Bay (King George Island), Antarctica: evidence for small-scale community structuring

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The Antarctic Peninsula's coastal benthic ecosystems are shaped by highly dynamic environmental drivers, hence high-resolution biodiversity studies across depth gradients are key for improve our understanding current impacts of drivers on benthic communities and future projections. Benthic megafauna and seaweeds were surveyed in Collins Bay, King George Island, using ROV video transects (10–80 m depth) and analysed for diversity and community composition in relation to environmental factors. Soft substrates dominated the area (82.44% of frames), and 157 taxa from 15 phyla were recorded, with Asteroidea occurring in 62.14% of sampled depths and *Odontaster validus* being the most frequently observed species. Benthic community composition differed significantly with depth, distance from the glacier, and substrate (PERMANOVA; depth: $F = 16.10$, $R^2 = 11.91\%$, $p < 0.001$; distance: $F = 20.38$, $R^2 = 5.03\%$, $p < 0.05$; substrate: $F = 7.20$, $R^2 = 2.66\%$, $p < 0.001$), with depth explaining the largest proportion of variation. Species richness showed distance-dependent depth responses: no significant depth-related changes occurred close to the glacier, richness peaked at intermediate depths (50–60 m) at intermediate distances (negative binomial GLMM, $p < 0.001$), and increased strongly with depth at sites furthest from the glacier ($p < 0.001$). Functional composition also varied along these gradients. Sessile filter feeders dominated deeper glacial-proximal habitats, while mobile taxa increased in relative abundance with distance from the glacier, although larval dispersal strategies remained invariant across depths and distances. Macroalgal assemblages were primarily structured by depth, with species richness declining significantly below 40–50 m across all distance categories. Overall, our findings demonstrate that glacial retreat-related processes modulate how bathymetry structures benthic biodiversity, generating strong small-scale heterogeneity within a single fjord. This study provides a fine-scale baseline for detecting future changes in Antarctic benthic ecosystems under ongoing climate-driven glacial change.

Keywords Cold-water benthos, Environmental drivers, Habitat heterogeneity, Functional diversity, Community composition

Benthic communities form the richest component of the Antarctic food web in terms of macrofaunal species diversity¹ and can potentially store 4.5k tonnes of carbon per year². Existing knowledge has shown that a key driver of fjordic benthic community structure affected is glacial meltwater, where sedimentation, turbidity, and ice-scour influence habitat characteristics, which is something that climate change is expected to affect and increase its effects, hence improving our understanding of current impacts of drivers on benthic communities is key for future projections³. Fjordic habitats further from glacial outflow typically experience lower sedimentation rates and have sandier substrates, whereas fjord habitats near glaciers are shaped by ice-scouring, high sedimentation, increased turbidity, and fine silty deposits interspersed with coarser glacially scoured substrates^{4,5}. Ice-scour, one of the most impactful physical disturbances on Earth⁶, is especially influential in shallow zones and further

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contributes to the patchy and heterogeneous nature of these near-glacier habitats by scraping the seafloor and removing organisms in its path^{7–10}.

Alongside this mechanical disturbance, sedimentation also has a significant influence on benthic diversity (e.g.¹¹); for instance, high sedimentation can have negative effects on pelagic, sessile and non-sessile benthic organisms^{12–15}. Additionally, it has been suggested that in deeper waters, where light availability diminishes, sedimentation becomes the dominant driver of benthic community structure¹⁶. These environmental conditions shape community complexity and functional trait dominance. In shallow waters, grazers and scavengers dominate, gradually transitioning to suspension feeders with increasing depth¹⁷, whereas in deeper waters, ascidians tend to be more abundant than sponges, which are otherwise dominant in Antarctic benthic communities^{18,19}. However, while such studies describe clear depth-related patterns, others have reported more complex and variable community structures that are strongly influenced by habitat heterogeneity^{20,21}.

To better understand how these environmental gradients and physical disturbances interact to shape benthic communities, particularly across depth and glacial influence, it is necessary to study fjords with contrasting geomorphological features. Fjords along the Antarctic Peninsula, including those around King George Island (KGI), Maritime Antarctica, display complex seabed morphologies shaped by repeated glacial advance and retreat, supporting diverse and often highly localised benthic communities^{8,21}. While comparative studies across fjords are essential at broader scales, here we adopt a within-fjord approach, using Collins Bay as a case study to examine how depth and proximity to a marine-terminating glacier structure benthic communities under a single geomorphological setting. KGI, located in the South Shetland Islands off the northern tip of the Antarctic Peninsula, hosts several fjordic inlets, including Marian Cove and Collins Bay. The latter, located on the island's western coast, is enclosed by a ~20 m sill that hinders the entrance of large icebergs, limiting deep ice-scouring. This provides a unique opportunity to study how glacial proximity and bathymetry shape benthic community structure without the confounding influence of icebergs from external sources. Despite the uniqueness of this opportunity, Collins Bay has not yet been the subject of studies that characterise its benthic biodiversity across a broad bathymetric gradient. In contrast, other areas such as Marian Cove have been extensively studied (see²²). Although the site has been included in previous work, it was only at low spatial or taxonomic resolution and without detailed bathymetric context^{23–25}. More broadly, there is a general lack of high-resolution datasets that link biological communities with oceanographic conditions along the West Antarctic coast⁴. This is particularly important as environmental gradients in Antarctic fjords often vary gradually with depth and distance from glacial sources, potentially leading to transitional shifts in community composition rather than abrupt faunal zonation²⁶ contradicting earlier works describing clear zonation patterns. Addressing these knowledge gaps is critical for assessing the impacts of climate-driven glacial retreat on Antarctic benthic ecosystems.

This study aims to provide a high-resolution, baseline characterisation of benthic community structure in Collins Bay, examining the influence of glacial proximity and bathymetry on species composition, relative abundance, and diversity patterns of macrofauna and seaweeds. Specifically, we hypothesise that environmental gradients lead to a continuous shift in species composition and functional traits with depth, rather than a strict zonation in Collins Bay²⁶. We expect an increase in species abundance, species richness and functional diversity with depth and distance from the glacier^{22,30}. Additionally, mobile species are expected to be more prevalent in areas subject to higher disturbance near the glacier, facilitating recolonisation after episodic sedimentation events. Hence, we anticipate identifying distinct community assemblages along the bathymetric gradient, shaped by the interplay of glacial influence and seabed depth.

Results

A total of 673 frames were sampled in Collins Bay at depths that ranged between 10.2 and 78.8 m depth. Soft substrates dominated the study area, accounting for 82.44% of all frames across stations (Fig. 1). At individual stations, soft sediments were also the most prevalent, reaching 100% at A3, B2, C1, and C2, and exceeding 85% at A1, B1, B3, BC, and C4. Pebble and cobble substrates occurred predominantly at station C3 and A4, boulder substrates were rare, detected only once at station A4 (Fig. 1; Supplementary Table 1).

General diversity patterns

A total of 5,489 presences were recorded, 3,638 of which corresponded to megafauna, representing 15 phyla and 157 unique taxa (Fig. 1). Among the megafauna, the class Asteroidea appeared in most frames (364) and was found at 62.14% of sampled depths. *Odontaster validus* was the most frequently observed species, with 229 presences across 42.71% of sampled depths. The second most abundant animal taxon was morphologically identified as *Newnesia* sp., with 198 presences recorded across 35.54% of all depths sampled. Two other abundant taxa included a Terebellid (152 presences) and a small, unidentifiable Polychaeta (145 presences). Three species, the bivalve *Laternula elliptica* and the polychaetes *Newnesia* sp., and a Terebellid, were present at all twelve sampled stations. The deepest and most versatile species were Terebellids, which occurred at 78.87% of the sampled depths. The remaining 1,851 presences consisted of benthic algae and were counted in a presence-absence manner. The most abundant seaweed species, *Ulothrix* sp., was counted 399 times in 62.92% of the depth range. This was followed by *Himantothallus grandifolius* ($n = 295$) at 45.78% of the depth range, and diatomaceous films ($n = 161$), at 33.76%. At the phylum level, seaweeds included members of Chlorophyta (418 frames present), Ochrophyta (412), Rhodophyta (244), and CrCA (128).

Benthic community patterns

At close proximity sites, the benthic community showed a high spread of phyla, with Mollusca (C3: 56.02%; $n = 121$; B1: 55.75%; $n = 97$), Echinodermata (C3: 22.69%; $n = 49$; B1: 13.22%; $n = 23$), and Porifera (C3: 13.43%; $n = 29$; B1: 10.34%; $n = 18$) dominating in the shallow waters of stations C3 and B1 (Fig. 2). In the deeper waters of stations C1 and C2, the community shifted to Chordata, dominantly the class Ascidacea, accompanied by

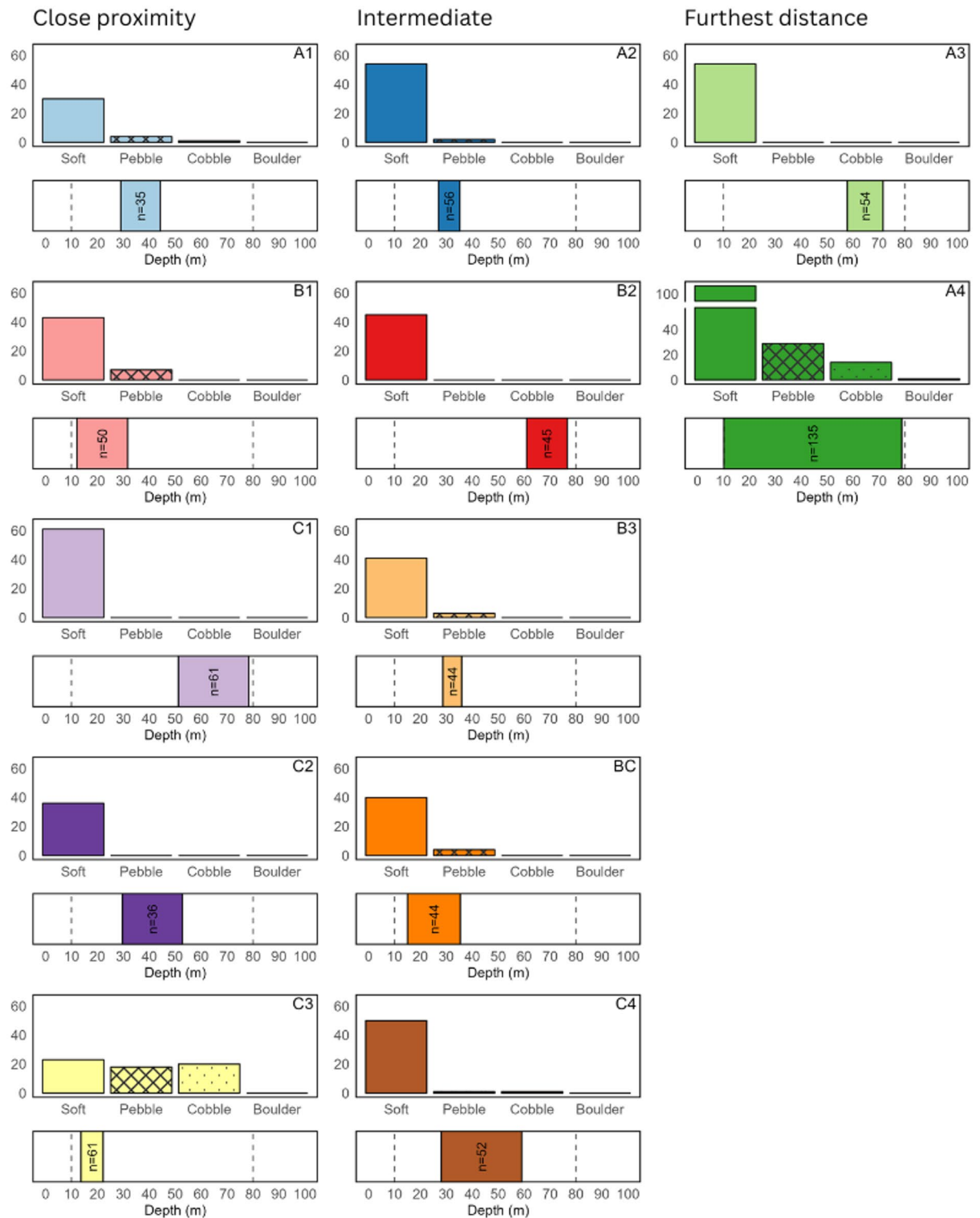


Fig. 1. Overview of each station (noted in top right corner) sampled at Collins Bay, King George Island. Top graph for each station shows substrate type counted per frame. Bottom graph for each station shows depth range of the frames (n) of that station, within total range of the study (dashed lines). Stations are divided into three distance categories: close proximity, intermediate and furthest distance from Collins Glacier. The dashed lines indicate the minimum and maximum sampling depth.

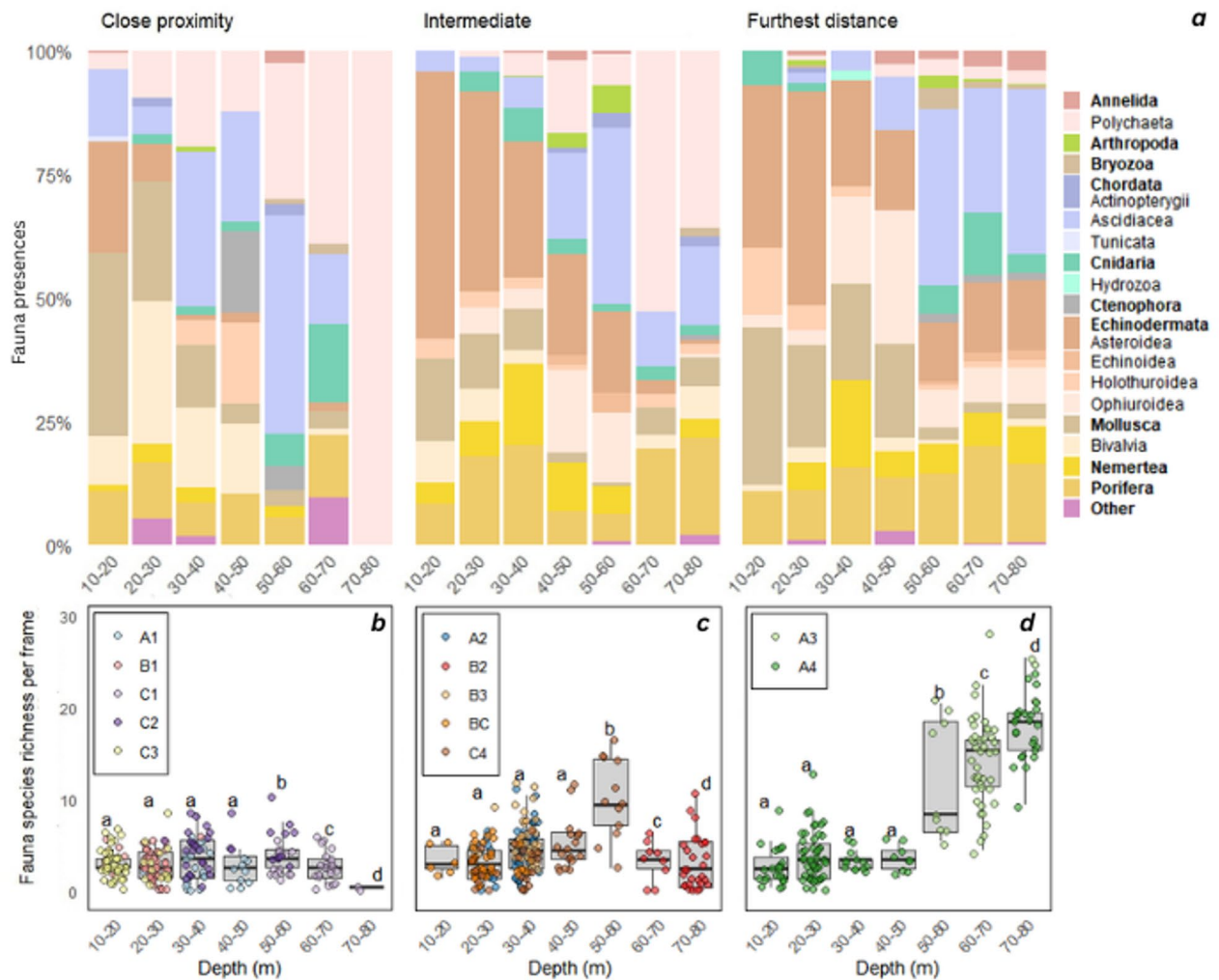


Fig. 2. Top panel shows proportions of faunal phyla (a) depth ranges of all stations (Fig. 7), Phyla are in bold and classes in regular text underneath. Depths are binned in 10 m intervals and divided over distance from the glacier in Collins Bay, King George Island. Bottom panels show faunal species richness per frame y depth, divided into close proximity to the glacier (b), intermediate proximity to the glacier (c) and furthest distance from the glacier (d). Colour separates stations. Depths sharing the same letter do not differ significantly in species richness within a given distance class (negative binomial GLMM, Holm-adjusted post hoc tests).

Cnidaria (C1: 13.18%; $n=17$) and Annelida (only Polychaeta; C2: 28.80%; $n=55$). In the deepest zone, Porifera disappeared likely due to low sampling numbers between 70 and 80 m ($n=10$). No significant differences in richness were detected across depths at these sites, although a trend of increasing richness with depth was observed (NB GLMMs: all z -ratios < 2 , $p > 0.05$).

At intermediate distances, benthic animals were dominated by Echinodermata (B3: 42.80%; $n=113$; BC: 62.42%; $n=103$), with increasing contributions from Porifera (B3: 21.97%; $n=58$; BC: 10.30%; $n=17$) and Ascidacea/Chordata (B2: 16.20%; $n=23$; C4: 24.92%; $n=74$) with depth. Here, richness significantly increased from shallow to mid-depths (10–20 m vs. 50–60 m: $z = -4.257$, $p < 0.001$; 20–30 m vs. 50–60 m: $z = -7.744$, $p < 0.001$; 30–40 m vs. 50–60 m: $z = -6.766$, $p < 0.001$), and then decreased again in deeper waters (50–60 m vs. 60–70 m: $z = 4.388$, $p < 0.001$; 50–60 m vs. 70–80 m: $z = 5.505$, $p < 0.001$).

At the furthest distance, shallow waters at station A4 showed a much higher proportion of Porifera (A4: 26.00%; $n=75$), while species richness dramatically increased with depth, with Chordata (A3: 26.32%; $n=215$) and Echinodermata (A3: 24.72%; $n=202$) forming the major groups, and Porifera remaining important in deeper waters (A3: 18.73%; $n=153$). Significant increases in richness were detected between shallow and deep depths (10–20 m vs. 50–60 m: $z = -6.015$, $p < 0.001$; 10–20 m vs. 60–70 m: $z = -7.563$, $p < 0.001$; 10–20 m vs. 70–80 m: $z = -13.751$, $p < 0.001$), indicating a strong depth-driven diversification at sites furthest from the glacier.

At close proximity sites, community composition exhibited clear and consistent patterns with depth. In shallow waters, the benthos were characterised by a high contribution of macroalgae, especially Ochrophyta (C3: 42.58%; $n=109$; B1: 30.71%; $n=43$) and Chlorophyceae (C3: 19.92%; $n=51$; B1: 46.43%; $n=65$; Fig. 3b). With increasing depth, CrCA became progressively more dominant (C1: 88.89%; $n=16$; C2: 9.80%; $n=5$), while the relative contribution of other algal groups declined. This shift in dominant functional groups was accompanied

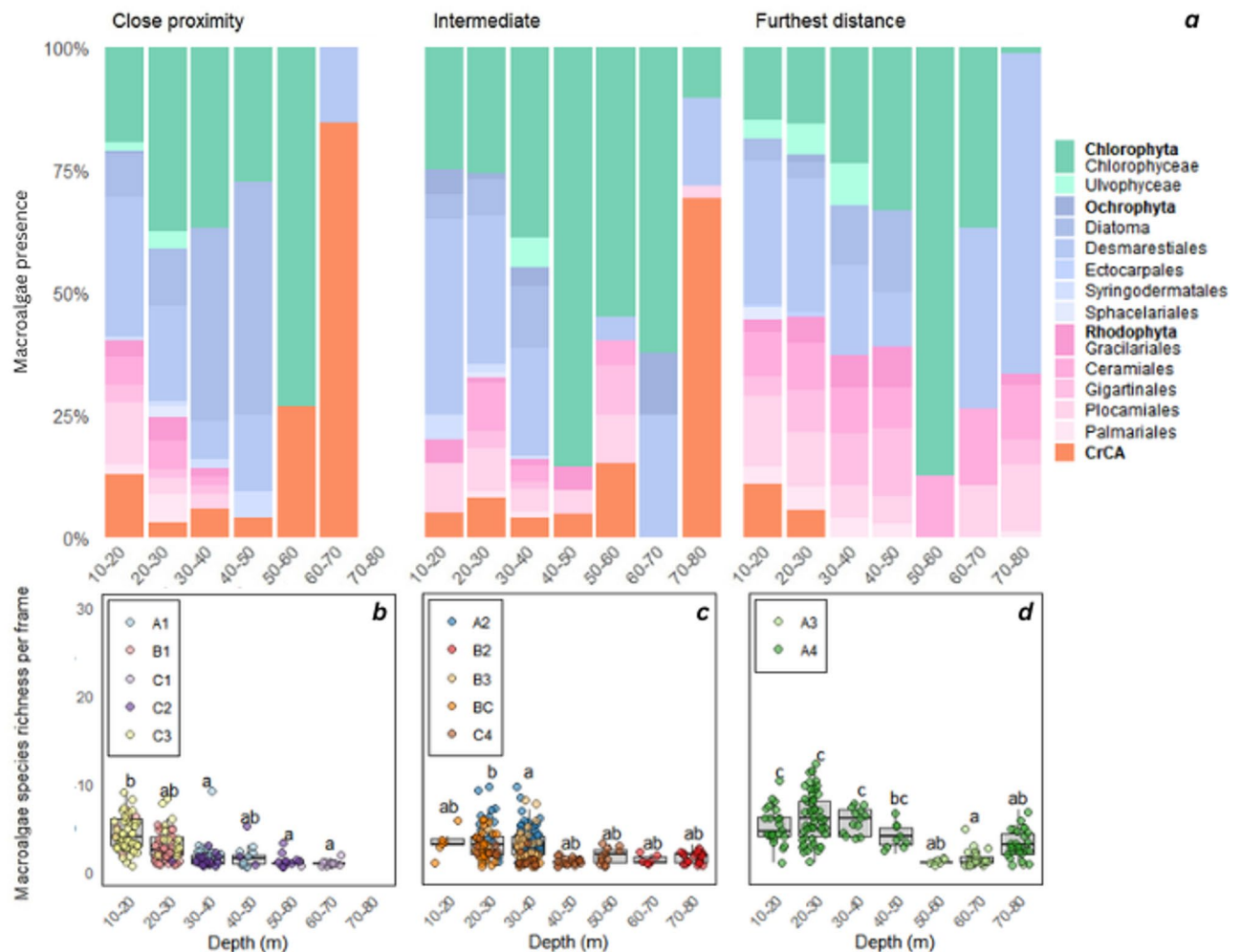


Fig. 3. Top panel shows proportions of macroalgae phyla and diatoms (a) over the depth ranges of all stations, phyla are in bold and classes in regular text underneath. Depths are binned at 10 m intervals and divided over distance from the glacier in Collins Bay, King George Island. Bottom panels show species richness per frame divided into close proximity to the glacier (b), intermediate proximity to the glacier (c) and furthest distance from the glacier (d). Colour separate stations. Depths sharing the same letter do not differ significantly in macroalgal species richness within a given distance class (negative binomial GLMM, Holm-adjusted post hoc tests).

by a marked reduction in overall diversity with depth (10–20 m vs. 30–40 m: $z = 3.417$, $p < 0.01$; 10–20 m vs. 50–60 m: $z = 3.367$, $p < 0.05$; 10–20 m vs. 60–70 m: $z = 3.150$, $p < 0.05$).

At intermediate distances, Ochrophyta generally dominated (A2: 41.08%; $n = 99$; B3: 49.25%; $n = 66$; BC: 42.11%; $n = 48$), accompanied by Chlorophyceae (A2: 37.34%; $n = 90$; B3: 32.09%; $n = 43$; BC: 30.70%; $n = 35$) and Rhodophyta (A2: 17.84%; $n = 43$; BC: 20.18%; $n = 23$). At some stations (B2, C4), CrCA became the main contributor (B2: 57.45%; $n = 27$; C4). A significant decrease in richness was observed from 20 to 30 m to 30–40 m ($z = 3.291$, $p < 0.05$), while other depth contrasts were not statistically significant.

At the furthest distance, shallow waters of stations A3 and A4 showed dominance of Ochrophyta (A4: 41.59%; $n = 272$) and Chlorophyceae (A3: 40.38%; $n = 21$; A4: 16.97%; $n = 111$), along with Rhodophyta (A3: 25.00%; $n = 13$; A4: 36.09%; $n = 236$). Deeper waters continued to show high abundance of the same groups, with significant richness decreases between shallow and deep depths (Fig. 3d). Species richness in shallow waters (< 40 m) was significantly higher than in deeper waters, with both 10–20 m and 20–30 m differing strongly from depths > 50 m (e.g. 10–20 m vs. 50–60 m: $z = 3.405$, $p = 0.0086$; 10–20 m vs. 60–70 m: $z = 4.089$, $p = 0.0008$; 20–30 m vs. 60–70 m: $z = 4.858$, $p < 0.0001$). In contrast, no significant differences were detected among shallow depths (< 40 m), supporting a clear separation between shallow and deeper benthic communities at the furthest distance.

Community changes within stations

Depth was found to be a significant structuring factor at stations A2, A3, B2, C2, and C4, with depth bin explaining 7–24% of the observed variation and no evidence of heterogeneous multivariate dispersion, indicating that

these differences reflect shifts in mean community composition rather than variation in within-bin variability (Table 1). Several additional stations (A4, B1, BC, and C1) also exhibited significant results; however, these stations showed significant heterogeneity in multivariate dispersion (A4: $F_{135,3}=6.19, p<0.001$; B1: $F_{50,3}=7.74, p<0.001$; BC: $F_{44,3}=3.20, p<0.05$; C1: $F_{52,3}=13.02, p<0.001$), suggesting that apparent differences among depth bins may be influenced by unequal community variability rather than true depth-related compositional changes. At the remaining stations (A1, B3, C3), no significant differences among depth bins were detected.

Community changes in the entire bay

Faunal community composition differed significantly among depth bins, substrate types, and distance from the glacier (Depth: $F=16.10, p<0.001$; Substrate: $F=7.20, p<0.001$; Distance: $F=20.38, p<0.05$). Depth had the largest effect, explaining 11.91% of the variation, followed by distance (5.03%) and substrate (2.66%). However, tests for homogeneity of multivariate dispersions indicated that depth and substrate exhibited significant differences in dispersion among groups, meaning that some of the observed differences may reflect unequal variability within each station rather than differences in mean community composition. In contrast, dispersion was homogeneous among the three distance categories, supporting a robust effect of distance.

Canonical component analysis

The CCA model partitioned the total scaled Chi-square inertia of 6.24 into constrained (0.88; 14.17%) and unconstrained (5.36; 85.83%) components (Fig. 4). The first canonical axis (CCA1) had an eigenvalue of 0.42, explaining 6.44% of total inertia, with cumulative proportions for the first two axes reaching 10.01%. Constrained eigenvalues showed that CCA1 accounted for 46.88% of the variation explained by environmental variables, with the first two axes together representing 70.62% of the constrained variation.

Species scores indicated variation in associations with environmental gradients. For example, the classes Echinoidea and Ophiuroidea had positive scores on CCA1 (1.29 and 1.08, respectively), while Tunicata and Gastropoda were negative (−1.53 and −0.83, respectively). Across CCA2, Annelida (classes otherwise undefinable) and Hexactinellida showed positive values (0.80 and 0.51, respectively), whereas Polychaeta (idem) and Bivalvia (idem) were negative (−0.87 and −0.80, respectively).

CCA1 was strongly influenced by temperature, density, depth, and distance from the glacier. Temperature exhibited a strong negative loading on CCA1 (−0.88), whereas density (0.77), depth (0.76), and the furthest distance from the glacier (0.72) had strong positive loadings, indicating that communities at warmer, shallower, and more proximal sites differed markedly from those in colder, deeper, and more distant locations. Substrate type also contributed to CCA1, with soft substrate positively associated (0.47) and pebble substrate negatively associated (−0.35).

CCA2 was less strongly structured but reflected additional environmental variation. The factor most strongly associated with CCA2 was proximity to the glacier, with the closest sites having a strongly negative centroid (−0.83), while the furthest (0.52) and intermediate distance sites (0.38) showed positive associations. Salinity and substrate type contributed only minor loadings on CCA2 (salinity: −0.02; pebble: 0.02; soft: −0.05), suggesting that the second axis captured variation related primarily to spatial positioning rather than water column properties.

Mobility and functional traits

Adult mobility differed slightly with depth showing significant differences only in the close proximity and intermediate distance categories. At close proximity of Collins Glacier, mobility at 10–20 m was significantly higher than at 30–40 m ($z=3.37, p<0.05$), 50–60 m ($z=3.24, p<0.05$) and 60–70 m ($z=3.12, p<0.05$), while other pairwise contrasts were not significant. In the intermediate distance group, mobility at 20–30 m was

Station	Frames	Number of depth bins	F-value	R2	P-value	P-value dispersion
A1	35	3	0.73	0.04	0.81	0.00
A2	56	2	4.87	0.08	0.00	0.73
A3	54	3	1.87	0.07	0.01	0.10
A4	135	5	14.57	0.31	0.00	0.00
B1	50	3	3.12	0.12	0.00	0.00
B2	45	2	4.04	0.09	0.01	0.09
B3	44	2	1.12	0.03	0.35	0.04
BC	44	3	4.42	0.18	0.00	0.02
C1	52	3	3.71	0.13	0.00	0.00
C2	36	4	2.02	0.16	0.01	0.15
C3	61	2	1.84	0.03	0.07	0.30
C4	52	4	5.04	0.24	0.00	0.16

Table 1. PERMANOVA results testing for differences in benthic community composition among depth bins within each station. Frames indicate the number of unique replicates included per station. F-value, R², and p-value are from the PERMANOVA; P-value dispersion corresponds to the test for homogeneity of multivariate dispersion. Significant results are in bold.

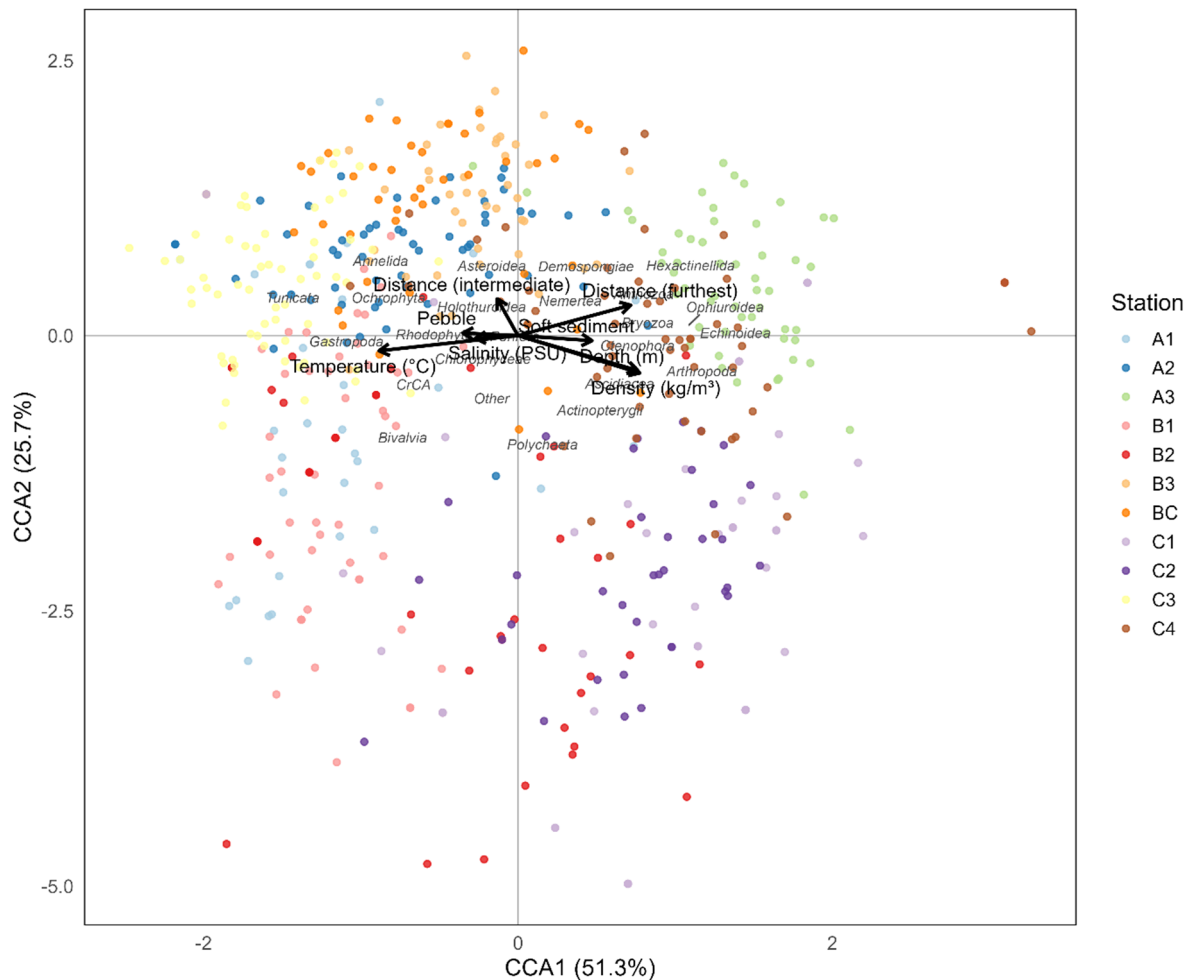


Fig. 4. Canonical component analysis (CCA) of classes of fauna and seaweeds present in Collins Bay, King George Island. Species without precise taxonomic information are classed within the parent phylum. Vectors represent environmental variables.

significantly lower than at 70–80 m ($z=3.29$, $p<0.05$) and mobility at 30–40 m was higher than at 70–80 m ($z=3.47$, $p<0.05$). In contrast, no significant differences were detected in the furthest distance.

Community-weighted mean values of larval dispersal showed no significant differences across depths or between glacial distance groups (Fig. 5, bottom). Larval type composition remained consistent regardless of proximity to the glacier, indicating that dispersal strategy is not influenced by distance from the ice margin in this system Fig. 6.

Functional feeding modes varied significantly with depth (PERMANOVA; $F_{649,6} = 19.49$; $p<0.001$) and substrate ($F_{649,3} = 14.05$; $p<0.05$) but not with distance ($F_{649,2} = 27.16$; $p=0.32$). In areas close to the glacier, opportunists and filter feeders dominated the benthic community. In the 10–20 m depth bin, opportunists accounted for 38.78% ($n=76$) of feeding modes, predators 23.47% ($n=46$), and filter feeders 18.88% ($n=37$). At slightly deeper waters (30–40 m), filter feeders became increasingly prominent 62.16% ($n=115$) of presences, while opportunists contributed 28.11% ($n=52$). Overall, filter feeders made up most feeding modes in waters near the glacier.

At intermediate distances, opportunists remained the dominant group across most depth bins, reaching 61.54% ($n=136$) in the 20–30 m bin and 52.33% ($n=269$) in the 30–40 m bin, while filter feeders accounted for 23.53% ($n=52$) and 31.52% ($n=162$), respectively. Predators contributed 10.41–12.65% between 20- and 40-m depth.

Further from the glacier, the community composition shifted: opportunists and filter feeders still contributed substantially, but predators and grazers became more prominent. In shallow waters (10–20 m), opportunists made up 46.05% ($n=35$), predators 27.63% ($n=21$), and grazers 14.47% ($n=14$), while filter feeders accounted for only 10.53% ($n=8$). In deeper waters (60–70 m) filter feeders comprised 55.18% ($n=346$), opportunists 29.67% ($n=186$), and predators 14.19% ($n=89$).

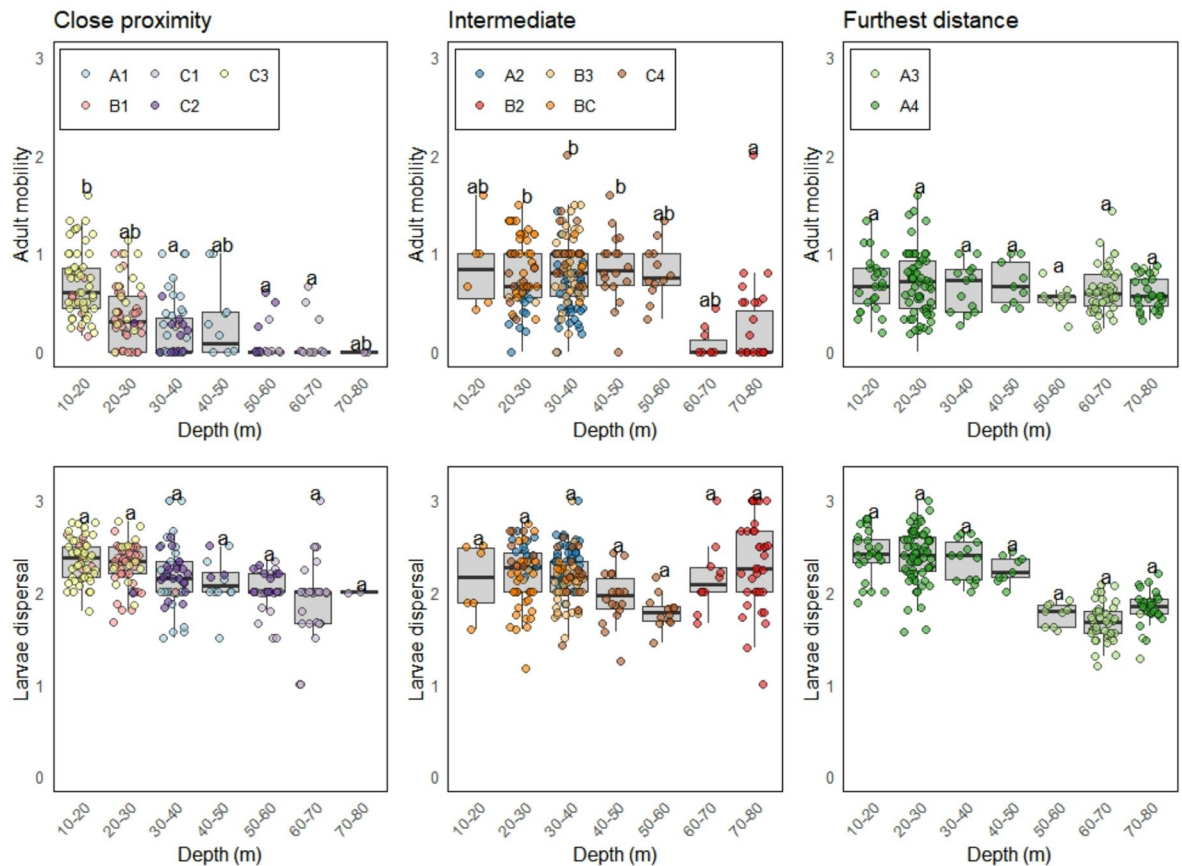


Fig. 5. Boxplots showing adult mobility (top) and larval type (bottom) by depth, categorised into three glacial distance groups. Mobility and larval type values were derived using fuzzy coding, following Vandewalle et al.³¹ (Supplementary Tables 2 and 3). Letters indicate statistically significant differences between groups based on post hoc pairwise comparisons (Tukey-adjusted, $p < 0.05$) after NB GLMM. Stations are divided into three distance categories: close proximity, intermediate and furthest distance from Collins Glacier.

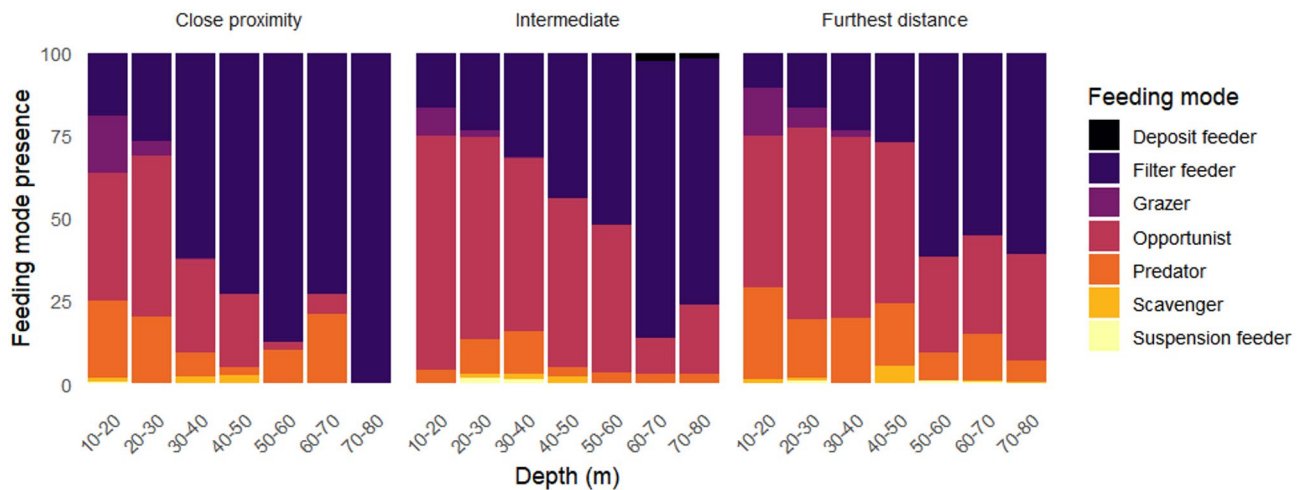


Fig. 6. Functional feeding modes in benthic organisms over distance from the glacier and depth based on trait data from Vandewalle et al.³¹ (Supplementary Tables 2 and 3). Stations are divided into three distance categories: close proximity, intermediate and furthest distance from Collins Glacier.

Discussion

This study provides the first detailed assessment of shallow-water benthic biodiversity in Collins Bay, a site located in one of the most active areas in the Antarctic, in terms of human activities³² but which has remained relatively understudied^{23–25,33}. Our 2024/2025 summer results showed how bathymetry and glacial proximity are the main factors influencing species composition and functional traits. No strict species zonation was observed, supporting the hypothesis that environmental gradients drive continuous rather than discrete zones in benthic community structures²⁶. The absence of depth-related structuring reflects gradual shifts in assemblage composition across depths, superimposed on strong small-scale patchiness. Despite the relatively small spatial extent of the surveyed area in Collins Bay, we found considerable heterogeneity throughout stations and depths, supporting the hypothesis that fine-scale environmental variability within the fjord shape the benthos rather than large-scale processes^{5,34–36}.

The patterns observed in this study align with broader regional findings while offering new insights into fine-scale biodiversity dynamics. A similar study within Maxwell Bay by Kim et al.²² documented spatial variation in benthic megafauna structure and function across Marian Cove, adjacent to Collins Bay, driven by depth and distance from the glacier. Although their results reflect comparable patterns, the degree of heterogeneity reported there was somewhat less pronounced. This difference may stem from sill structure, Marian Cove has a clear sill limiting iceberg intrusion and thus disturbance, a similar sill is present – but far less pronounced – in Collins Bay. Therefore, the difference in heterogeneity might be due to disturbance, similarly as found by Rovelli et al.⁵ in Doumer Island.

Our survey revealed three times the number of seaweed taxa reported previously by Valdivia et al.²⁵, and double the number reported by Newcombe & Cárdenas²³ in the same study area, underscoring the strength of video surveys in capturing algal diversity as well as its capacity to survey a greater area, when compared with the previous studies using dredge sampling or quadrats taken by SCUBA divers. Valdivia et al.²⁵ reported water turbidity to be higher near the surface and concluded it as a potential explanation for the observed increased diversity at greater depths. Several studies have shown that sedimentation exerts multiple stressors on benthic communities^{37,38}, including increased mineral discharge, which can induce oxidative stress and metal accumulation in filter feeders (e.g.³⁹), as well as reduce food availability and clog feeding structures^{40,41}. In Collins Bay, richness patterns varied with both depth and distance from the glacier, suggesting that glacier-related effects are not uniform across the fjord but interact with bathymetry. Contrary to previous observations, species richness did not globally increase with depth close to the glacier. Only in the stations furthest from Collins Glacier, it was recorded a sharp increase in species richness with depth as more filter feeders dominated the seafloor. This pattern was similarly noted as an explainable factor by Kim et al.²² in Marian Cove, an area which is adjacent to Collins Bay. Near to the glacier in shallow waters, a higher number of pioneer species such as molluscs (*L. elliptica* and *N. concinna*), ascidians and echinoderms (*O. validus* and *Neosmilaster* sp.) was recorded. The dominance of pioneer species such as molluscs is expected, as they can bury themselves and thus avoid ice impact, as noted in Potter Cove by Sahade et al.¹⁸. Furthermore, the mobility of echinoderms may allow them to actively seek favourable conditions. Similarly, the high relative abundance of ascidians near the glacier in deeper waters is in accordance with previous studies^{18,42} who reported a peak of ascidian density at around 30 m depth in Marian Cove and Potter Cove, respectively.

Although Antarctic coastal waters are generally well mixed, subglacial discharge from the marine-terminating Collins Glacier may locally alter circulation and enhance nutrient availability⁴³. Such discharge may carry nutrients, like iron, organic matter, and sediments from beneath the ice sheet^{44,45}, which interact with intrusions of relatively warmer subsurface waters during the flood time in the head of the bay⁴⁶, increasing phytoplankton biomass and primary production in nearshore areas⁴⁷ and supporting unexpectedly high presences close to glacier fronts due to pelagic-benthic coupling⁴⁸. However, it is also plausible that the discharge itself is driven by meteorological and oceanographic forcing, including wind and offshore intrusions of warm deep water⁴⁹, rather than acting as a primary driver of circulation. Further investigations into nutrient fluxes, chlorophyll concentrations and water column structure are needed to better understand the underlying processes.

The significance of primary producers in shaping benthic communities cannot be underestimated. Larger macroalgal species can facilitate the establishment of benthic organisms in highly disturbed areas⁵⁰. In this study, areas with high macroalgal presence co-occurred with elevated benthic diversity, suggesting a potential facilitative role, although causal mechanisms cannot be resolved from observational data alone. In contrast, diatoms and filamentous algal aggregates serve as essential food sources in Antarctic ecosystems, impacting energy transfer throughout the benthic food web⁵¹. In addition to their ecological function, diatoms are increasingly recognised as sensitive indicators of environmental change, particularly concerning glacial influence⁵². In Collins Bay, their abundance peaked at intermediate depths (20–40 m) and declined with increasing depth, mirroring patterns reported in Marian Cove, King George Island⁵³ and South Bay, Doumer Island⁵⁴. These studies describe massive blooms of filamentous colonial diatoms at similar depths, where environmental conditions are favourable for growth. The higher diatom presence in glacially influenced zones of Collins Bay may likewise reflect nutrient pulses or stabilised substrates in areas of moderate disturbance. Such blooms are thought to be linked to changing salinity, temperature, and stratification caused by ice melt^{52–54}. Their rapid response to environmental variability highlights benthic diatoms as valuable indicators of ecosystem change, with future shifts in primary production and food-web structure likely to follow patterns of glacial retreat.

The widespread distribution of diverse algal assemblages, particularly Desmarestiales and Chlorophyceae, suggests that primary productivity remains relatively high despite glacial influence. This aligns with the findings of Quartino et al.⁵⁵, who observed that macroalgal community structure in Antarctic coastal environments is primarily shaped by depth, substrate type, and irradiance, with salinity and nutrient availability playing a lesser role. Ice scouring further contributes to spatial patchiness in these communities. In Collins Bay, species richness generally declined with increasing depth, consistent with reduced irradiance as a limiting factor (e.g.⁵⁶).

Interestingly, furthest from the glacier, a slight increase in algal richness was observed at the deepest depths, possibly reflecting reduced ice disturbance, which is similar to what was found by Quartino et al.⁵⁵ in Potter Cove, the eastern part of KGI. Despite this, no clear trend emerged concerning glacial distance, suggesting that spatial heterogeneity and patchiness play a significant role in structuring local algal diversity, something that has been demonstrated by other studies in the WAP⁵. For example, shallow stations near the glacier (A1, B1, and C3) hosted diverse communities, including Desmarestiales, Chlorophyceae, and diatomaceous films. However, *Palmaria decipiens*, a known glacial opportunist found in Marian Cove^{57,58}, Half Moon Island⁵⁹, and Potter Cove⁵⁵, and even found in deep waters⁶⁰, was relatively scarce (relative abundance: < 5%) in our study. This challenges expectations that pioneer species would dominate these extreme environments and suggests that local conditions may favour a broader range of algal ecological baselines for future shifts in benthic community structure. Notably, recent observations by Amsler et al.⁵² revealed rapid shifts in macroalgal cover in the Palmer Archipelago over just four years, emphasising that Antarctic seaweed communities are highly dynamic, which could be an alternative reasoning for the presented findings, as the study encompassed only one season.

Beyond species richness, the depth gradient exhibited a clear effect on functional groups, with mobile taxa becoming increasingly present further from the glacier. In high-disturbance environments near glaciers, mobile species are generally expected to dominate due to their ability to recolonise after episodic sedimentation events¹⁷, and we indeed found a higher number of mobile taxa – including arthropods, echinoderms, and nemertean – in the more shallow waters close to the glacier, while deeper waters were dominated by sessile, filter feeding fauna. This pattern likely reflects a combination of the low adult mobility of filter feeders, and the relatively low disturbance frequency in deeper habitats⁶¹. Filter feeders, widespread in deeper KGI sites⁶², can increase local heterogeneity by providing additional surface for colonisation¹⁸, which helps explain the observed peak in faunal species richness at 50–60 m depth due to the higher relative abundance of Ascidacea there. In Collins Bay, where over 83% of frames consist of soft sediment and show no significant correlation between species distribution and substrate type, the diversity of filter feeders reinforces the high patchiness typical of Antarctic fjord ecosystems^{5,26,63}. Along the gradient away from the glacier, the increasing presence of mobile taxa with corresponds to a higher number functional groups present, reflecting environmental drivers such as reduced disturbance and increased resource availability²², rather than a direct causal effect of taxa on ecosystem function.

In many marine benthic systems, increasing disturbance leads to declines in long-lived, structurally important taxa, while disturbance-tolerant, mobile species dominate in high-disturbance areas (e.g.^{60,64}). In Collins Bay, however, sessile taxa remained dominant even in deeper glacial-proximal habitats, suggesting site-specific differences in disturbance regimes or resource availability. While highly disturbed environments are often associated with species exhibiting pelagic larval development due to their rapid recolonisation potential^{65,66}, our findings indicate no difference in reproductive strategies across depths or distances. While some studies have examined broad-scale patterns such as the latitudinal gradient⁶⁷, the influence of substrate on functional groups^{30,68}, or large-scale patterns in Arctic regions³¹, high-resolution studies that compare local functional diversity along depth and glacier gradients remain largely absent. The findings presented here thus provide a valuable baseline for understanding functional diversity within small-scale studies.

Collins Bay is highly dominated by soft sediments, both across the bay and within most individual stations, with hard substrates such as pebbles, cobbles, and boulders occurring only locally, most notably at stations C3 and A4. This relative homogeneity in substrate composition indicates that much of the observed spatial variation in benthic communities develops against a broadly uniform sedimentary background. Consequently, depth and distance from the glacier emerge as the primary environmental gradients structuring benthic assemblages, while substrate plays a secondary and more context-dependent role. Although substrate type contributed significantly to variation in community composition at the scale of the entire bay, its effect was weaker than that of depth and distance and was partly associated with increased heterogeneity rather than consistent shifts in mean community structure. This suggests that in soft-bottom Antarctic fjord systems such as Collins Bay, vertical and glacial gradients override substrate effects in shaping benthic biodiversity, particularly where structural complexity is limited.

Conclusions

This study provides the first fine-scale assessment of benthic biodiversity in Collins Bay, revealing how bathymetry and proximity to the glacier are key interacting drivers of community composition. Benthic assemblages showed distance-dependent depth responses, with weak depth structuring close to the glacier, mid-depth richness peaks at intermediate distances, and strong depth-related increases in richness at sites furthest from the ice margin. These patterns indicate that glacial influence modulates how bathymetry structures benthic communities rather than imposing uniform effects across the bay. Community composition varied significantly among stations and depth bins, while macroalgal assemblages were primarily structured by depth, showing consistent richness declines with increasing depth across all distance categories. Functional analyses revealed dominance of sessile filter feeders in deeper glacial-proximal habitats, with mobile taxa becoming more prevalent further from the glacier, whereas larval dispersal strategies remained invariant. Iceberg scouring might contribute to local heterogeneity, creating local patchy habitats. Given the rapid pace of glacial retreat in the Antarctic Peninsula^{69,70}, continued monitoring of benthic communities in Collins Bay is essential for tracking ecosystem responses to climate-driven environmental change, especially in areas with a high human footprint^{33,71}. High-resolution biodiversity assessments such as this provide a crucial baseline for future conservation efforts and improve our understanding of how Antarctic benthic ecosystems will adapt to a changing climate.

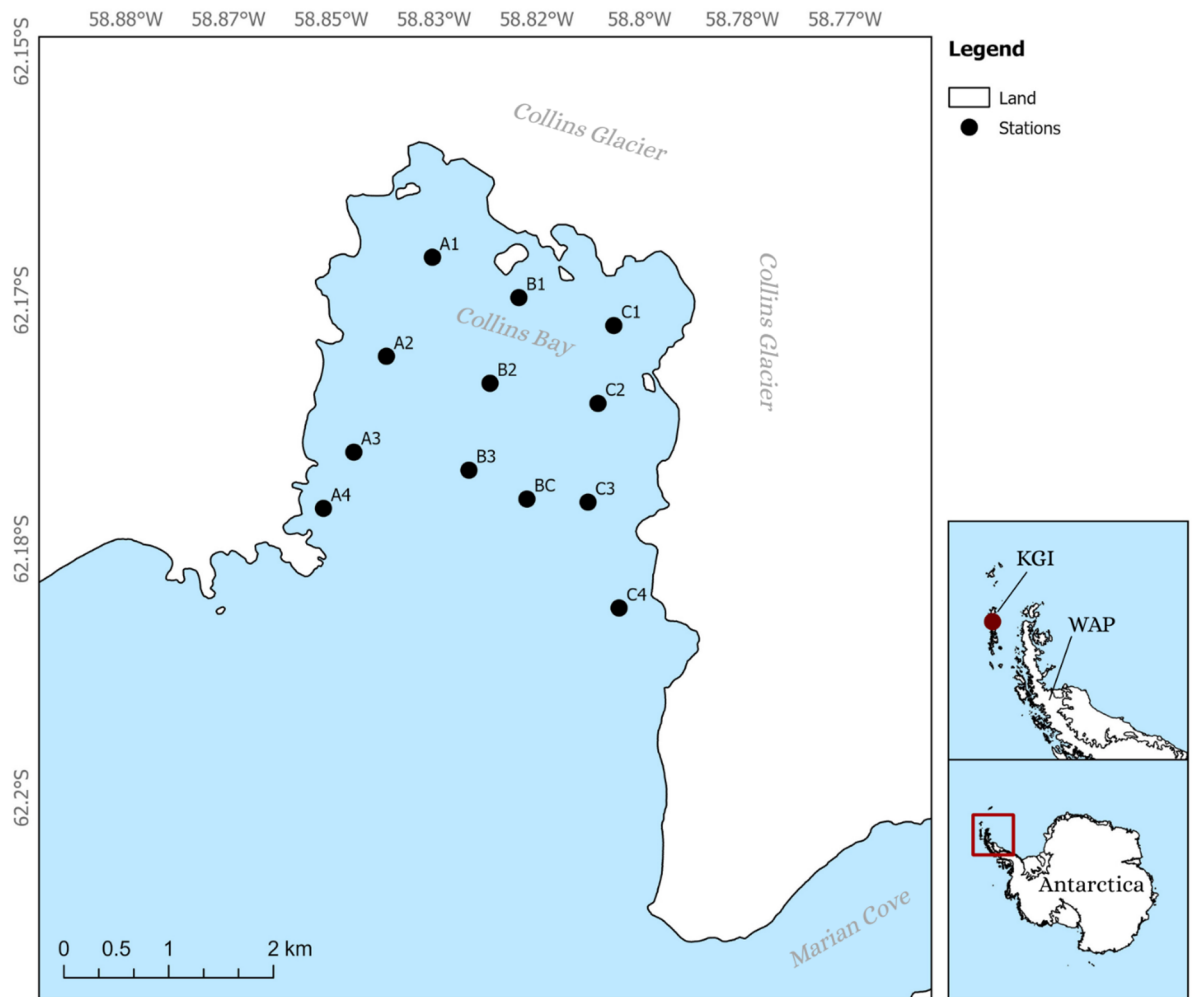


Fig. 7. Sampling area of Collins Bay, King George Island (KGI) in the Western Antarctic Peninsula (WAP) with Collins Glacier in the South-East of Maxwell Bay. Antarctic coastline via Gerrish et al.⁷² and bathymetry of South Shetland Islands via Fremant⁷³.

Methods

Study site

Sampling was conducted in December 2024 in Collins Bay (62.177°S, 58.826°W), a semi-enclosed cove approximately 3 × 3 km in size, located within Maxwell Bay, one of the two major fjords systems on King George Island, South Shetland Islands (Fig. 7). The bay reaches depths of up to 190 m at the central part of its mouth. Collins Glacier, a small ice dome covering approximately 15 km² with a maximum elevation of 270 m, influences the southeastern region of the bay⁷⁴. The glacier's catchment area spans roughly 50 km², and it directly influences the adjacent coastal zone through both land-terminating and tidewater-terminating fronts⁷⁵. Stations were selected in Collins Bay to ensure that each depth profile (10–90 m depth) overlapped as well as possible with each distance from the glacier (ranging from 0 to 3 km). The distance from the glacier was calculated using ArcGIS Pro by getting the shortest distance between the station location and the glacier. Stations were then divided into three distance categories (close proximity, intermediate and furthest away).

ROV surveying procedures

To assess biodiversity non-invasively, twelve ROV video surveys were conducted in December 2024 in Collins Bay using the FIFISH V6 EXPERT and FIFISH V6 PRO by QYSEA & FiFish. Both ROVs were equipped with a UHD 4K underwater camera (12-megapixel resolution, 166° ultra-wide field of view) flanked by two 6000-lumen LED lights to ensure consistent illumination. In each station, the transect included at least 35 frames, captured with the ROV positioned at a stable 0.5 m height above the seafloor to avoid disturbing the sediment. Each transect followed a butterfly survey consisting of two radial transects separated by ~60°, creating two equilateral triangle with a maximum radius of 50 m from a central starting point where the Zodiac was anchored, or in deeper waters, kept at the same coordinates.

Video analysis

A total of 678 frames were distinguished from the video-transects of 12 stations (Fig. 7). For each frame, depth from the ROV screen and substrate type were recorded. Substrate was determined as the most prominent – covering more than half of the visible seafloor within the frame – categorised as soft, pebble, cobble, or boulder. All recognisable epibenthic megafauna (approximately > 1 cm) were counted and identified to the lowest possible taxonomic level using standard flora and fauna guides^{76–78,79} and online databases (e.g. www.marinespecies.org, www.fishbase.se). Colonial species were counted as one, except when physically separated by sediment or other organisms. Due to the inability to distinguish individual thalli in video imagery, seaweeds were not quantified as discrete individuals. Instead, we use the term seaweed as an overarching term including macroalgae, encrusting coralline algae (CrCa) and benthic diatoms films (considered as one taxon following the approach used by other authors (Deregibus et al. 2024) enabling comparison with faunal groups in subsequent analyses.

Environmental data

Conductivity–temperature–depth (CTD) profiles were recorded using a DST CTD by Star Oddi while the ROV conducted transects to capture in-situ water characteristics. Measurements were taken every ten seconds during descent. Sensor accuracies for conductivity, temperature, and salinity were ± 1.5 mS/cm, ± 0.1 °C, and ± 0.1 PSU, respectively, while the depth accuracy, determined via pressure, was $\pm 0.6\%$ over the entire range. Consequently, the first 0.5 m of measurements (from the bottom) were removed from the dataset. Salinity was calculated as practical salinity (PSS-78) from conductivity, and similarly, potential density anomaly (σ in kg/m³) and potential temperature (θ in °C) were derived from the CTD data.

To capture water characteristics unaffected by daily fluctuations, all stations were sampled in a clockwise sequence, using a SonTek CastAway[®] CTD. This device offers an accuracy of ± 0.05 °C and ± 0.1 PSU, operates at a 5 Hz sampling rate, and includes an integrated GPS for georeferenced casts.

Data analysis

Univariate analyses of species richness

Species richness of animals and plants was analysed separately using generalised linear mixed modelling. Richness was modelled as a function of distance from the glacier (categorised as close proximity, intermediate, and furthest distance), depth (binned), and their interaction. Distance categories were treated as an ordered categorical factor to preserve their spatial interpretation. To account for the hierarchical sampling design and non-independence among samples, station was included as a random effect nested within distance.

Since species richness data were counts and exhibited overdispersion, a negative binomial error distribution was used. Model fit was assessed using simulation-based residual diagnostics. Residual distributions were visually inspected to evaluate departures from expected patterns, including skewness, zero inflation, and non-linearity. Formal tests based on simulated residuals were used to assess whether residuals conformed to the assumed distribution, providing an indirect assessment of normality on the model scale. Heterogeneity of variance was evaluated by examining residual dispersion across fitted values and across levels of the explanatory factors. No substantial violations of model assumptions were detected.

Post-hoc comparisons were conducted using estimated marginal means calculated on the response scale. Pairwise contrasts among depth bins were performed separately within each distance category. To control for multiple testing, p-values were adjusted using the Holm correction. Compact letter displays were used to summarise statistically significant differences among depth bins within each distance category.

Multivariate community composition analyses

Community composition analyses were based on presence/absence data aggregated at the replicate level. Taxon counts were summed per replicate and taxonomic unit, then reshaped into a community matrix with replicates as rows and taxa as columns. Replicates with zero total abundance and taxa absent across all samples were removed prior to analysis to avoid artefacts in distance calculations. For analyses focusing on species occurrence rather than abundance, the community matrix was converted to presence–absence format. Associated metadata were compiled for each replicate, including station, depth bin, distance, and substrate type.

To test the effect of environmental factors on the benthic community, differences in community composition were assessed using permutational multivariate analysis of variance (PERMANOVA). For presence–absence data, Jaccard dissimilarity was used, whereas Bray–Curtis dissimilarity was applied to abundance-based analyses. The global PERMANOVA model tested for the effects of substrate type, depth bin, and distance on community composition and their interaction. Permutation tests were constrained within stations to respect the sampling design and avoid pseudo replication. Statistical significance was assessed using 999 permutations. Because PERMANOVA is sensitive to differences in within-group dispersion, the assumption of homogeneity of multivariate dispersion was explicitly tested prior to interpretation of results. For each explanatory factor (substrate, depth bin, and distance), multivariate dispersion was calculated as the distance of samples to their group centroid in multivariate space. Differences in dispersion among groups were evaluated using both an analysis of variance on distances to centroids and a permutation test. Boxplots were used as a supplementary visual check.

To assess whether community composition differed among depth bins within individual stations, PERMANOVA was performed separately for each station. For each station, abundance data were aggregated per replicate and taxon, and Bray–Curtis dissimilarity matrices were calculated. Depth bin was used as the sole explanatory variable. Stations with fewer than three replicates or fewer than two depth bins were excluded from this analysis. For each station-specific PERMANOVA, test statistics, explained variance (R^2), and p-values were extracted. In parallel, homogeneity of dispersion among depth bins was tested within each station using

permutation tests. Station-level results were only considered robust where dispersion did not differ significantly among depth bins.

To assess similarity among stations based on environmental conditions, environmental variables were standardised and pairwise Euclidean distances among stations were calculated. Hierarchical clustering using average linkage was applied to identify groups of environmentally similar stations. Principal component analysis was used to visualise major environmental gradients and to identify variables driving station clustering, with particular attention to the role of depth relative to other physical parameters.

Differences in substrate composition and biological community structure were examined explicitly. Substrate composition was analysed using abundance-based dissimilarities and tested using PERMANOVA, with dispersion tests used to confirm homogeneity of variance. Similarly, species composition at the class level was compared between selected stations using Bray–Curtis dissimilarity, PERMANOVA, and dispersion tests. Non-metric multidimensional scaling was used as a complementary visualisation to illustrate similarities and differences in species composition between stations. Dominant taxa contributing most to observed differences were identified by ranking total abundances within each station.

*Constrained ordination analysis (CCA)*⁸⁰

To examine relationships between community composition and environmental variables, constrained ordination was conducted using abundance data aggregated at the class level. Replicates were aligned with corresponding environmental data, including temperature, salinity, density, depth, substrate type, and distance from the glacier²⁵. Replicates with missing environmental data were excluded, and only samples with non-zero total abundance were retained. Environmental variables were used in their original units, with categorical substrate variables encoded as factors. Continuous environmental variables were assessed for collinearity prior to inclusion in the model. Canonical correspondence analysis was used to relate community composition directly to measured environmental gradients. The significance of the overall CCA model was tested using permutation tests. Marginal effects of individual environmental variables were assessed using term-by-term permutation tests, and the significance of canonical axes was evaluated separately. Ordination results were visualised using biplots displaying site scores, species scores, and environmental vectors. These plots were used to interpret ecological gradients structuring community composition and to identify taxa associated with specific environmental conditions.

Functional biodiversity analyses

Building on the above approaches, functional traits of organisms (e.g. adult mobility and larval type) were incorporated to further clarify community structure. The mean trait value per community (mT) was computed as a weighted average of species-specific trait values, with the species' relative abundances serving as weights:

$$mT = \sum_{i=1}^S p_i x_i$$

Here, x_i represents the trait value of the i -th species. For binary traits, x_i takes on values of 0 or 1. For categorical traits, a fuzzy coding method was used⁸¹ (Supplementary Table 1), where each taxon was assigned an affinity score (a_k) for each category ($1 \leq k \leq h$), with h being the total number of categories for the given trait. Affinity scores ranged from 0 (no affinity) to 3 (high affinity). These scores were converted into a frequency distribution by dividing each a_k by the total sum of the affinity scores for that taxon (see³¹ for further details). Trait information for faunal species was collected from Robinson et al.⁸² and adjusted to fit the observed taxa (Supplementary Tables 1 and 2). Community-weighted mean values of adult mobility and larval dispersal were analysed using generalised linear mixed models. Trait values were modelled as a function of depth bin, distance, and their interaction. Station was included as a random effect nested within distance category to account for spatial non-independence among replicates. Normality was formally assessed using Shapiro–Wilk tests applied to the raw mT values prior to modelling. Both traits deviated from normality, and mT values were bounded and heteroscedastic, precluding the use of Gaussian linear models. Consequently, models were fitted using a negative binomial error distribution with a log link. Model assumptions were evaluated using simulation-based residual diagnostics. Residual distributions were examined for deviations from expected patterns, including skewness, zero inflation, and non-linearity. Heterogeneity of variance was assessed by inspecting residual dispersion across fitted values and across levels of depth and distance. No systematic violations of model assumptions were detected. Post-hoc comparisons among depth bins were conducted separately within each distance category using estimated marginal means calculated on the response scale. Pairwise contrasts were adjusted for multiple testing using the Holm correction. Compact letter displays were used to summarise statistically significant differences.

Feeding mode structure was examined using complementary univariate and multivariate approaches. First, relative abundances of feeding modes were calculated per depth bin and distance and expressed as percentages of total abundance. Presence-based summaries were also generated to identify the most frequently occurring feeding modes within each depth–distance combination, reducing the influence of highly abundant taxa. To formally test for differences in feeding mode composition across environmental gradients, a multivariate analysis was performed using a presence–absence matrix of feeding modes per replicate. Dissimilarity among replicates was calculated using Jaccard distance. Differences in feeding mode composition were tested as a function of substrate type, depth bin, and distance using permutational multivariate analysis of variance, with permutations constrained within stations.

Because permutational multivariate analyses are sensitive to differences in within-group dispersion, homogeneity of multivariate dispersion was explicitly tested prior to interpretation. Dispersion was quantified

as the distance of each replicate to its group centroid in multivariate space. Differences among groups were assessed using both parametric and permutation-based tests. Only results for factors that met the assumption of homogeneous dispersion were interpreted as reflecting differences in functional composition rather than variance structure.

Functional trait analyses were interpreted alongside taxonomic composition and environmental gradients to provide a mechanistic understanding of community structure along depth and distance gradients. By combining trait-based metrics with multivariate community analyses, this approach allows differentiation between compositional turnover driven by species replacement and shifts in dominant ecological strategies.

All data processing and statistical analyses were performed in R (RStudio 2023.06.2, build 561).

Data availability

All data are available in the main text or the Supplementary Information.

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References

- Griffiths, H. J. Antarctic marine biodiversity – What do we know about the distribution of life in the Southern Ocean?. *PLoS One* **5**, e11683 (2010).
- Morley, S. A. et al. Benthic biodiversity, carbon storage and the potential for increasing negative feedbacks on climate change in shallow waters of the Antarctic Peninsula. *Biology* **11**, 320 (2022).
- Morley, S. A. et al. Global drivers on Southern Ocean ecosystems: Changing physical environments and anthropogenic pressures in an Earth system. *Front. Mar. Sci.* **7**, 547188 (2020).
- Jerosch, K. Benthic meltwater fjord habitats formed by rapid glacier recession on King George Island, Antarctica. *Philos. Trans. R. Soc. Lond. A Math. Phys. Eng. Sci.* <https://doi.org/10.1098/rsta.2017.0178> (2018).
- Rovelli, L., Attard, K. M., Cárdenas, C. A. & Glud, R. N. Benthic primary production and respiration of shallow rocky habitats: A case study from South Bay (Doumer Island, Western Antarctic Peninsula). *Polar Biol.* **42**, 1459–1474 (2019).
- Gutt, J. & Starmans, A. Quantification of iceberg impact and benthic recolonisation patterns in the Weddell Sea (Antarctica). *Polar Biol.* **24**, 615–619 (2001).
- Barnes, D. K. A. The influence of ice on polar nearshore benthos. *J. Mar. Biol. Assoc. U. K.* **79**, 401–407 (1999).
- Brown, K. M., Fraser, K. P. P., Barnes, D. K. A. & Peck, L. S. Links between the structure of an Antarctic shallow-water community and ice-scour frequency. *Oecologia* **141**, 121–129 (2004).
- Robinson, B. J. O., Barnes, D. K. A. & Morley, S. A. Disturbance, dispersal and marine assemblage structure: A case study from the nearshore Southern Ocean. *Mar. Environ. Res.* **160**, 105025 (2020).
- Robinson, B. J. O., Barnes, D. K. A., Grange, L. J. & Morley, S. A. Intermediate ice scour disturbance is key to maintaining a peak in biodiversity within the shallows of the Western Antarctic Peninsula. *Sci. Rep.* **11**, 16712 (2021).
- Barnes, D. K. A. & Souster, T. Reduced survival of Antarctic benthos linked to climate-induced iceberg scouring. *Nat. Clim. Chang.* **1**, 365–368 (2011).
- Slattery, M. & Bockus, D. Sedimentation in McMurdo Sound, Antarctica: A disturbance mechanism for benthic invertebrates. *Polar Biol.* **18**, 172–179 (1997).
- Eiane, K. & Daase, M. Observations of mass mortality of *Themisto libellula* (Amphipoda, Hyperidae). *Polar Biol.* **25**, 396–398 (2002).
- Fuentes, V. et al. Glacial melting: an overlooked threat to Antarctic krill. *Sci. Rep.* **6**, 27234 (2016).
- Giesecke, R., Höfer, J., Vallejos, T. & González, H. E. Death in southern Patagonian fjords: Copepod community structure and mortality in land- and marine-terminating glacier-fjord systems. *Prog. Oceanogr.* **174**, 162–172 (2019).
- Cárdenas, C. A. & Montiel, A. The influence of depth and substrate inclination on sessile assemblages in subantarctic rocky reefs (Magellan region). *Polar Biol.* **38**, 1631–1644 (2015).
- Smale, D. A. Ecological traits of benthic assemblages in shallow Antarctic waters: Does ice scour disturbance select for small, mobile, secondary consumers with high dispersal potential?. *Polar Biol.* **31**, 1225–1231 (2008).
- Sahade, R., Tatián, M., Kowalke, J., Kühne, S. & Esnal, G. B. Benthic faunal associations on soft substrates at Potter Cove, King George Island, Antarctica. *Polar Biol.* **19**, 85–91 (1998).
- Downey, R. V., Griffiths, H. J., Linse, K. & Janussen, D. Diversity and distribution patterns in High Southern Latitude Sponges. *PLOS One* **7**, e41672 (2012).
- Thatje, S., Hillenbrand, C.-D. & Larter, R. On the origin of Antarctic marine benthic community structure. *Trends Ecol. Evol.* **20**, 534–540 (2005).
- Post, A. L., Beaman, R. J., O'Brien, P. E., Eléaume, M. & Riddle, M. J. Community structure and benthic habitats across the George V Shelf, East Antarctica: Trends through space and time. *Deep Sea Research Part II: Topical Studies in Oceanography* **58**, 105–118 (2011).
- Kim, D. U., Ahn, I.-Y., Noh, J., Lee, C. & Khim, J. S. Shifts in benthic megafauna communities after glacial retreat in an Antarctic fjord. *Commun. Earth Environ.* **5**, 1–11 (2024).
- Newcombe, E. M. & Cárdenas, C. A. Rocky reef benthic assemblages in the Magellan Strait and the South Shetland Islands (Antarctica). *Rev. Biol. Mar. Oceanogr.* **46**, 177–188 (2011).
- Friedlander, A. M. et al. Spatial patterns of continental shelf faunal community structure along the Western Antarctic Peninsula. *PLOS One* **15**, e0239895 (2020).
- Valdivia, N., Garrido, I., Bruning, P., Piñones, A. & Pardo, L. M. Biodiversity of an Antarctic rocky subtidal community and its relationship with glacier meltdown processes. *Mar. Environ. Res.* **159**, 104991 (2020).
- Smale, D. A. Continuous benthic community change along a depth gradient in Antarctic shallows: Evidence of patchiness but not zonation. *Polar Biol.* **31**, 189–198 (2008).
- Zamorano, J. H. Zonación y biomasa de la macrofauna bentónica en bahía south, archipiélago de palmer, antártica. *Serie científica - Instituto Antártico Chileno* 27–38 (1983).
- Gambi, M. C., Lorenti, M., Russo, G. F. & Scipione, M. B. Benthic associations of the shallow hard bottoms off Terra Nova Bay, Ross Sea: Zonation, biomass and population structure. *Antarct. Sci.* **6**, 449–462 (1994).
- Barnes, D. & Brockington, S. Zoobenthic biodiversity, biomass and abundance at Adelaide Island, Antarctica. *Mar. Ecol. Prog. Ser.* **249**, 145–155 (2003).
- Convey, P. et al. The spatial structure of Antarctic biodiversity. *Ecol. Monogr.* **84**, 203–244 (2014).
- Vandewalle, M. et al. Functional traits as indicators of biodiversity response to land use changes across ecosystems and organisms. *Biodivers. Conserv.* **19**, 2921–2947 (2010).

32. McCarthy, A. H., Peck, L. S. & Aldridge, D. C. Ship traffic connects Antarctica's fragile coasts to worldwide ecosystems. *Proc. Natl. Acad. Sci. U. S. A.* **119**, e2110303118 (2022).
33. Salinas, C. X., Cárdenas, C. A., González-Aravena, M., Rebolledo, L. & Cruz, F. S. Mapping scientific fieldwork data: A potential tool for improving and strengthening Antarctic Specially Protected Areas as an effective measure for protecting Antarctic biodiversity. *Biodivers. Conserv.* **33**, 929–948 (2024).
34. Clarke, A. Benthic marine habitats in Antarctica. *Ecol. Res. West. Antarct. Peninsula* **70**, 129 (1996).
35. Ragua-Gil, J. M., Gutt, J., Clarke, A. & Arntz, W. E. Antarctic shallow-water mega-epibenthos: Shaped by circumpolar dispersion or local conditions? *Mar. Biol.* **144**, 829–839 (2004).
36. Grimes, C. J. et al. Benthic community heterogeneity on the Eastern Antarctic continental shelf. *Polar Biol.* **48**, 35 (2025).
37. Sahade, R. et al. Climate change and glacier retreat drive shifts in an Antarctic benthic ecosystem. *Sci. Adv.* **1**, e1500050 (2015).
38. Clark, G. F., Stark, J. S., Palmer, A. S., Riddle, M. J. & Johnston, E. L. The roles of sea-ice, light and sedimentation in structuring shallow Antarctic benthic communities. *PLOS ONE* **12**, e0168391 (2017).
39. Husmann, G. et al. The influence of sedimentation on metal accumulation and cellular oxidative stress markers in the Antarctic bivalve *Laternula elliptica*. *Estuar. Coast. Shelf Sci.* **111**, 48–59 (2012).
40. Krzeminska, M. & Kuklinski, P. Biodiversity patterns of rock encrusting fauna from the shallow sublittoral of the Admiralty Bay. *Mar. Environ. Res.* **139**, 169–181 (2018).
41. Topçu, N. E. et al. Impact of excessive sedimentation caused by anthropogenic activities on benthic suspension feeders in the Sea of Marmara. *J. Mar. Biol. Ass.* **99**, 1075–1086 (2019).
42. Kim, D.-U., Khim, J. S. & Ahn, I.-Y. Patterns, drivers and implications of ascidian distributions in a rapidly deglaciating fjord, King George Island, West Antarctic Peninsula. *Ecol. Indic.* **125**, 107467 (2021).
43. Meire, L. et al. Marine-terminating glaciers sustain high productivity in Greenland fjords. *Glob. Chang. Biol.* <https://doi.org/10.1111/gcb.13801> (2017).
44. Gerringa, L. J. A. et al. Iron from melting glaciers fuels the phytoplankton blooms in Amundsen Sea (Southern Ocean): Iron biogeochemistry. *Deep Sea Res. Part II Top. Stud. Oceanogr.* **71–76**, 16–31 (2012).
45. Death, R. et al. Antarctic ice sheet fertilises the Southern Ocean. *Biogeosciences* **11**, 2635–2643 (2014).
46. Llanillo, P. et al. Oceanographic variability induced by tides, the intraseasonal cycle and warm subsurface water intrusions in Maxwell Bay, King George Island (West-Antarctica). *Sci. Rep.* **9**, 18571 (2019).
47. Höfer, J. et al. The role of water column stability and wind mixing in the production/export dynamics of two bays in the Western Antarctic Peninsula. *Prog. Oceanogr.* **174**, 105–116 (2019).
48. Braeckman, U. Glacial melt impacts carbon flows in an Antarctic benthic food web. *Front. Mar. Sci.* <https://doi.org/10.3389/fmars.2024.1359597> (2024).
49. Meredith, M. P. et al. Anatomy of a glacial meltwater discharge event in an Antarctic cove. *Philos. Trans. R. Soc. Lond. A Math. Phys. Eng. Sci.* **376**, 20170163 (2018).
50. Cárdenas, C. A. et al. Sponge richness on algae-dominated rocky reefs in the western Antarctic Peninsula and the Magellan Strait. *Polar Res.* **35**, 30532 (2016).
51. Sporta Caputi, S. et al. Seasonal Food Web Dynamics in the Antarctic Benthos of Tethys Bay (Ross Sea): Implications for Biodiversity Persistence Under Different Seasonal Sea-Ice Coverage. *Front. Mar. Sci.* **7**, (2020).
52. Amsler, C. D. et al. Substantial short-term increases in brown macroalgal cover and total macroalgal biomass with decreased sea ice on the Western Antarctic Peninsula. *Mar. Ecol. Prog. Ser.* **759**, 17–34 (2025).
53. Ahn, I.-Y., Moon, H.-W., Jeon, M. & Kang, S.-H. First record of massive blooming of benthic diatoms and their association with megabenthic filter feeders on the shallow seafloor of an Antarctic fjord: Does glacier melting fuel the bloom? *Ocean Sci. J.* **51**, 273–279 (2016).
54. Morales, S., Cárdenas, C. A., Bravo-Gómez, D. & Lagger, C. Shallow hard-bottom benthic assemblages of South Bay (Antarctic Peninsula): An update 40 years later. *Diversity* **16**, 162 (2024).
55. Quartino, M. L., Zaixso, H. E. & Zaixso, A. Biological and environmental characterization of marine macroalgal assemblages in Potter Cove, South Shetland Islands, Antarctica. *botm* **48**, 187–197 (2005).
56. Deregibus, D. et al. Photosynthetic light requirements and vertical distribution of macroalgae in newly ice-free areas in Potter Cove, South Shetland Islands, Antarctica. *Polar Biol.* **39**, 153–166 (2016).
57. Chung, H., Oh, Y. S., Lee, I. K. & Kim, D. Y. Macroalgal Vegetation of Maxwell Bay in King George Island, Antarctica. *Algae* **9**, 47–58 (1994).
58. Ko, Y. W. et al. The glacier melting process is an invisible barrier to the development of Antarctic subtidal macroalgal assemblages. *Environ. Res.* **233**, 116438 (2023).
59. Neushul, M. Diving observations of sub-tidal Antarctic marine vegetation. *Bot. Mar.* **8**, 234–243 (1965).
60. Robinson, B. J. O. et al. New confirmed depth limit of Antarctic macroalgae: *Palmaria decipiens* found at 100 m depth in the Southern Ocean. *Polar Biol.* **45**, 1459–1463 (2022).
61. Gutt, J. On the direct impact of ice on marine benthic communities, a review. *Polar Biol.* **24**, 553–564 (2001).
62. Piepenburg, D., Schmid, M. K. & Gerdes, D. The benthos off King George Island (South Shetland Islands, Antarctica): Further evidence for a lack of a latitudinal biomass cline in the Southern Ocean. *Polar Biol.* **25**, 146–158 (2002).
63. Gutt, J. & Starmans, A. Structure and biodiversity of megabenthos in the Weddell and Lazarev Seas (Antarctica): Ecological role of physical parameters and biological interactions. *Polar Biol.* **20**, 229–247 (1998).
64. Włodarska-Kowalczyk, M., Pearson, T. H. & Kendall, M. A. Benthic response to chronic natural physical disturbance by glacial sedimentation in an Arctic fjord. *Mar. Ecol. Prog. Ser.* **303**, 31–41 (2005).
65. Pearse, J. S., McClintock, J. B. & Bosch, I. Reproduction of Antarctic benthic marine invertebrates: Tempos, modes, and timing. *Integr. Comp. Biol.* **31**, 65–80 (1991).
66. Ziegler, A. F., Hahn-Woernle, L., Powell, B. & Smith, C. R. Larval dispersal modeling suggests limited ecological connectivity between fjords on the West Antarctic Peninsula. *Integr. Comp. Biol.* **60**, 1369–1385 (2020).
67. Wan Hussin, W. M. R., Husin, A., Syed Mahdzar, S. F. & Mohd Nadzir, M. S. Preliminary investigation on the structural, taxonomic and functional diversities of benthic communities at different areas in the West Antarctic Peninsula. *Polar Sci.* **20**, 100–106 (2019).
68. Mohd Nasir, N., Barnes, D. K. A. & Wan Hussin, W. M. R. Benthic functionality under climate-induced environment changes offshore on the Antarctic Peninsula continental shelf. *Mar. Environ. Res.* **194**, 106341 (2024).
69. Turner, J. et al. Antarctic climate change and the environment: An update. *Polar Rec.* **50**, 237–259 (2014).
70. Nel, W., Hedding, D. W. & Rudolph, E. M. The sub-Antarctic islands are increasingly warming in the 21st century. *Antarct. Sci.* **35**, 124–126 (2023).
71. Perterra, L. R., Hughes, K. A., Vega, G. C. & Olalla-Tárraga, M. Á. High resolution spatial mapping of human footprint across Antarctica and its implications for the strategic conservation of avifauna. *PLoS One* **12**, e0168280 (2017).
72. Gerrish, L., Ireland, L., Fretwell, P. *Cooper High resolution vector polylines of the Antarctic coastline.* <https://doi.org/10.5285/567c0911-83a0-493c-9dc7-15245c1c5f5e> (2024).
73. Fremant, A. A bathymetric compilation of the South Shetland Islands, 1991–2017 - British Antarctic Survey. <https://doi.org/10.5285/37cafd85-e84f-416c-8c09-51a5ec9b001c> (2019).
74. Simões, C. L., Rosa, K., Czapela, F. F., Vieira, R. & Simões, J. C. Collins glacier retreat process and regional climatic variations, King George Island, Antarctica. *Geogr. Rev.* **105**, 462–471 (2015).

75. Munoz, Y. P. & Wellner, J. S. Seafloor geomorphology of western Antarctic Peninsula bays: A signature of ice flow behaviour. *The Cryosphere* **12**, 205–225 (2018).
76. Bruggeman, P. *Underwater Field Guide to Ross Island & McMurdo Sound, Antarctica* (The National Science Foundation's Office of Polar Programs, 1998).
77. Ocampo, I. G. *Flora Marina Antártica* (Kultrún, 2015).
78. Rauschert, M. & Arntz, W. *Antarctic Macrobenthos: A Field Guide of the Invertebrates Living at the Antarctic Seafloor* (Girzig+Gottschalk GmbH, 2015).
79. Schories, D. & Kohlberg, G. *Marine Wildlife King George Island Antarctica*. (2016).
80. ter Braak, C. J. F. Canonical Correspondence Analysis: A new eigenvector technique for multivariate direct gradient analysis. *Ecology* **67**, 1167–1179 (1986).
81. Chevene, F., Dolédec, S. & Chessel, D. A fuzzy coding approach for the analysis of long-term ecological data. *Freshw. Biol.* **31**, 295–309 (1994).
82. Robinson, B. J. O., Barnes, D. K. A., Grange, L. J. & Morley, S. A. The extremes of disturbance reduce functional redundancy: Functional trait assessment of the shallow Antarctic benthos. *Front. Mar. Sci.* <https://doi.org/10.3389/fmars.2021.797112> (2022).

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Author contributions

D.B.J. and C.A.C. conceived the study. D.B.J. and A.H.S. conducted field sampling. D.B.J. performed the video analysis, numerical analysis, creation of figures and tables and writing the manuscript. C.A.C., M.G.A., F.S.C., and M.L. reviewed and edited the overall content of the manuscript. All the authors have been involved with the work and have approved the manuscript for submission.

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Declarations

Competing interests

The authors declare no competing interests.

Additional information

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