

Benthic mollusc assemblages in West Antarctica: taxa composition and ecological insights

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Abstract. Although different studies in Antarctica have dealt with benthic communities, few studies have focused on molluscan assemblages and their ecology. During the austral summer of 2011, 17 stations between depths of 68.5 and 754 m were sampled in West Antarctica using a demersal bottom trawl pilot net on board RV *ARA Puerto Deseado*. In all, 1848 specimens of shelled molluscs were recorded. Gastropods were the most diverse group (species richness = 74) and bivalves were the most abundant ($n = 1344$). Shannon–Wiener diversity index values ranged between 0.58 and 2.99, with great variation at different stations. Cluster analysis using the Bray–Curtis coefficient showed three distinct assemblages types: one dominated by suspension feeders; a second with representatives from different trophic groups, including suspension feeders, grazers, scavengers, predators and deposit feeders; and a third, more differentiated, with few taxa and dominated by deposit feeders. Finally, multivariate analysis suggests that bivalves were more sensitive to temperature, whereas gastropods were more sensitive to depth.

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Introduction

Over the past few years, Antarctica and its biota have received increasing attention in relation to global climate change (Convey *et al.* 2009, Turner *et al.* 2014). Recently, Sahade *et al.* (2015) reported a marked change in a benthic Antarctic community that may be associated with current climate change. That study highlighted the increased sediment run-off triggered by glacier retreat as the potential causal factor. However, to address these effects, more research is needed in order to describe how these communities will respond to physical or biological factors in a region with evidence of recent climate warming.

Benthic molluscs, particularly bivalves and gastropods, are abundant and have a wide variety of life history traits and strategies, so an analysis of their assemblages would likely contribute to further understanding of the structure of the communities in which they live. However, in the West Antarctic region, few quantitative approaches have been centred on molluscan assemblages (e.g. Arnaud *et al.* 2001; Troncoso *et al.* 2007; Aldea *et al.* 2008; Troncoso and Aldea 2008). Arnaud *et al.* (2001) found considerable variations in diversity at different stations between 40- and 850-m depth around Livingston Island, Deception Island and in the Bransfield Strait. These authors recognised that the local quantitative or qualitative differences between molluscan assemblages could be related to sediment heterogeneity, as well as variations in food availability. In the Bellingshausen Sea, Troncoso *et al.* (2007) also found considerable variations in diversity of soft-bottom

molluscs at depths ranging from 90 to 3304 m, postulating depth and percentage of coarse sand as the environmental variables that better explain such distribution. Later, Aldea *et al.* (2008) studied the bathymetric distribution and trends in the diversity of gastropods and bivalves from the shelf to lower slope in West Antarctica from the South Shetland Islands to the Bellingshausen Sea and concluded that diversity patterns are complex for both groups, with no trends associated with depth. Moreover, Troncoso and Aldea (2008) emphasised the community structure of these mollusc assemblages and discussed potential physical and biological factors that could play a role in shaping their distribution.

Given global climate warming and recent environmental changes, as well as the need for updated ecological information on benthic communities, the present study provides new data on molluscan fauna in West Antarctica. The aim of this study was to characterise the structure of mollusc assemblages based on taxa composition, ecological parameters and environmental factors, with an emphasis on trophic groups due to the lack of previous information on this topic.

Materials and methods

Study area

The study area covered the region from the South Shetland Islands to the northern Antarctic Peninsula and the South Orkney Islands (Fig. 1). The South Shetland Islands and the

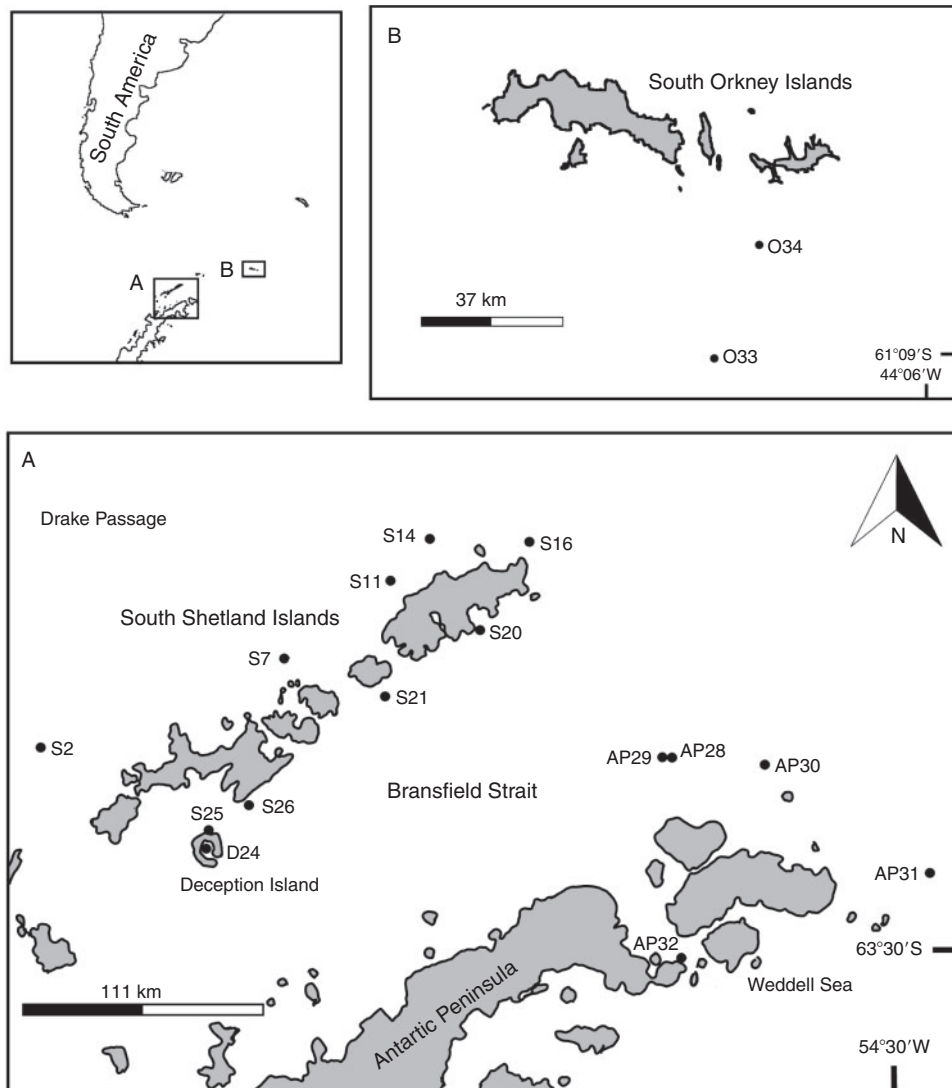


Fig. 1. Map showing the location of the study area and the sampling stations.

northern Antarctic Peninsula are located on the continental shelf and are separated by the Bransfield Strait, whereas the South Orkney Islands are a group of islands ~600 km north-east of the tip of the Antarctic Peninsula. This archipelago represents the emergent fragments of the southern part of the Scotia Arc.

Sampling

Samples were collected in the 2011 austral summer during the Antarctic Expedition CAV 2011 aboard the oceanographic survey ship *ARA Puerto Deseado*. In all, 17 stations at depths ranging from 68.5 to 754 m (Table 1; Fig. 1) were sampled using a demersal bottom trawl pilot net (total length 6 m, 25-mm mesh on the wings and 10-mm mesh in the cod end, vertical opening 0.6 m, horizontal aperture 1.8 m). Hauls were taken during both the day and night, with a target time for a bottom trawl of 15 min and a tow speed between 2 and 3.7 kn (~1.03 and ~1.9 m s⁻¹). Surface temperature and salinity data were measured using a

Seabird SBE 21 thermosalinograph (Sea-Bird Scientific, Bellevue, WA, USA) whereas depth in deep water was measured using a SIMRAD EA400 (Kongsberg Maritime, Horten, Norway) echo-sounder. Each sample is a single point in space at each site. Samples were preserved in 4% buffered formaldehyde.

Data collection and analyses

The mollusc specimens (living taxa along with articulated and well-preserved empty shells) were counted in order to estimate relative abundance. The identification and taxonomic position of mollusc taxa was performed following different authors and databases (see Appendix 1). For each mollusc taxa, the following feeding modes were considered: deposit feeder, suspension feeder, predator, scavenger and grazer.

For each sampling station, the total abundance (N) and species richness (S) of molluscs were recorded. To assess diversity and evenness, the Shannon–Wiener index (H') and Pielou's evenness

Table 1. Location of sampling stations and environmental factors measured
PSU, practical salinity units

Station	Latitude (S)	Longitude (W)	Depth (m)	Temperature (°C)	Salinity (PSU)
S2	62°27.4'	61°21.9'	186.5	2.3	33.8
S7	62°13.0'	59°41.6'	68.5	2.1	34.1
S11	61°56.0'	58°47.8'	206.5	2.4	34
S14	61°46.6'	58°26.1'	246.5	2.3	34
S16	61°49.6'	57°34.4'	210	1.7	34.1
S20	62°09.7'	58°03.4'	105	2.1	34
S21	62°22.3'	58°53.9'	122.5	2.1	33.8
D24	62°57.3'	60°37.7'	156.5	2.5	33.8
S25	62°52.4'	60°35.6'	213.5	2.2	33.9
S26	62°47.2'	60°12.3'	454	2.4	33.9
AP28	62°43.0'	56°32.0'	201.5	0.5	34.2
AP29	62°43.2'	56°29.8'	222	0.6	34.1
AP30	62°45.6'	55°37.2'	88	0.8	34.1
AP31	63°13.2'	54°08.0'	244	0.2	33.9
AP32	63°32.1'	56°26.2'	754	0.4	33.9
O33	61°10.0'	44°59.6'	166	2	33.8
O34	60°54.6'	44°46.9'	165	2.1	33.8

index (J') were calculated respectively. The evenness index is constrained between 0 and 1, with higher values representing more even distributions in abundance among taxa.

To identify the main assemblages, the Bray–Curtis similarity coefficient was applied to the data to obtain a similarity matrix. Hierarchical clusters were represented using a dendrogram (McKenna 2003). Gastropods and bivalves were treated separately in order to compare their patterns of distribution.

To test for differences between surveyed assemblages, an analysis of similitude (ANOSIM) was used. This analysis provides a test statistic, R , that varies between -1 and 1 , with 0 representing the null hypothesis of no differences within a set of samples. Generally, R lies between 0 and 1 , representing the magnitude by which samples differ. Finally, to identify the mollusc species responsible for the overall dissimilarity between groups of samples, the similarity percentage analysis (SIMPER) procedure was used.

A canonical correspondence analysis was also performed in order to identify the variation of trophic groups over stations in relation to three environmental variables (salinity, temperature and depth) following the guidelines and interpretations of ter Braak and Verdonschot (1995) and Legendre and Legendre (2012). For this analysis, physical data (water temperature, salinity, and depth) were log transformed ($x + 1$). Biological data were also standardized with a square root transformation. Rare species (those that only appeared at one station) were eliminated from the matrices to reduce noise in the dataset. All multivariate analyses were performed using PAST software (Hammer *et al.* 2001; see http://palaeo-electronica.org/2001_1/past/issue1_01.htm).

Finally, to characterise the population structure of two abundant bivalves, namely *Nuculana inaequisculpta* and *Yoldia eightsi*, under the specific conditions of volcanic activity on Deception Island, the size frequency distribution was calculated. Three linear measurements were taken on articulated specimens using an Essex digital calliper (0–150 mm; Cramerton, NC,

USA; see <http://essexmotorcycles.co.uk/vernier-caliper-digital-0-150mm-hgl-01-1>): shell height (maximum dorsoventral distance), shell length (maximum anteroposterior distance) and shell width (distance across the valves). The length size distribution was plotted on a frequency histogram. Mean values and dispersion estimations for the length, height and width of the shells were also calculated. A non-parametric Kolmogorov–Smirnov two-sample test was performed using PAST software (Hammer *et al.* 2001) to compare both distributions.

Results

Mollusc assemblages: abundance, richness and diversity

In all, 1848 shelled mollusc specimens belonging to four classes, 38 families and 108 species were recovered. Most were bivalves ($N = 1344$), followed by gastropods ($N = 446$), with scaphopods ($N = 51$) and chitons ($N = 7$) in lower proportions. However, the best-represented class in terms of species richness was the Gastropoda (74 species), followed by Bivalvia (31 species), Scaphopoda (two species) and Polyplacophora (one species). The gastropod families Trochidae (12 species), Buccinidae (12 species) and Turridae (11 species) were the most diverse.

Table 2 shows the taxonomic distribution of these four classes of molluscs over the stations. In total, 13 of 17 stations had less than 12 families, and only 3 stations (AP28, AP29 and S14) had 20 families. Station AP28 had a higher number of species (43 species) than AP29 (28 species). The stations with fewer families were S2 (5 species), D24 (5 species) and S7 (3 species), with only bivalves in the last two stations.

Species richness varied between five (in Stations S7, AP31, and O33) and 43 (AP28), with diversity indices between 0.58 and 2.99, thus showing considerable variation between different stations. The highest value of evenness was obtained at station S16 (0.94) and the lowest at station S11 (0.25), which indicates that these stations are the least and the most equal respectively (Table 3).

Table 2. Taxonomic composition of molluscs recovered for each sample

Station	Gastropoda	Bivalvia	Polyplacophora	Scaphopoda
S2	1 family (1 species)	3 families (5 species)	Absent	1 family (1 species)
S7	Absent	3 families (5 species)	Absent	Absent
S11	8 families (16 species)	7 families (12 species)	1 family (1 species)	1 family (1 species)
S14	10 families (19 species)	9 families (12 species)	Absent	1 family (1 species)
S16	7 families (12 species)	3 families (3 species)	Absent	Absent
S20	6 families (9 species)	3 families (3 species)	1 family (1 species)	Absent
S21	6 families (9 species)	4 families (4 species)	Absent	Absent
D24	Absent	5 families (6 species)	Absent	Absent
S25	5 families (9 species)	5 families (6 species)	Absent	1 family (1 species)
S26	3 families (5 species)	4 families (6 species)	1 family (1 species)	1 family (1 species)
AP28	10 families (27 species)	8 families (14 species)	1 family (1 species)	1 family (1 species)
AP29	11 families (18 species)	8 families (9 species)	1 family (1 species)	Absent
AP30	4 families (9 species)	2 families (3 species)	Absent	Absent
AP31	1 family (1 species)	3 families (3 species)	Absent	1 family (1 species)
AP32	7 families (10 species)	4 families (5 species)	Absent	Absent
O33	2 families (2 species)	2 families (2 species)	Absent	1 family (1 species)
O34	4 families (7 species)	5 families (5 species)	Absent	1 family (1 species)

Table 3. Relative abundance and diversity parameters

H' , Shannon–Wiener index; J' , Pielou's evenness index

Station	Richness	Abundance	Diversity (H')	Evenness (J')
S2	7	72	1.45	0.61
S7	5	13	1.04	0.57
S11	30	187	2.02	0.25
S14	32	170	2.94	0.59
S16	15	20	2.65	0.94
S20	13	75	1.88	0.50
S21	13	32	2.01	0.57
D24	6	584	0.70	0.34
S25	16	97	1.59	0.31
S26	13	30	2.32	0.78
AP28	43	209	3.31	0.62
AP29	28	63	2.99	0.71
AP30	12	23	2.35	0.88
AP31	5	29	1.13	0.62
AP32	15	30	2.34	0.69
O33	5	130	0.58	0.36
O34	13	84	1.70	0.42

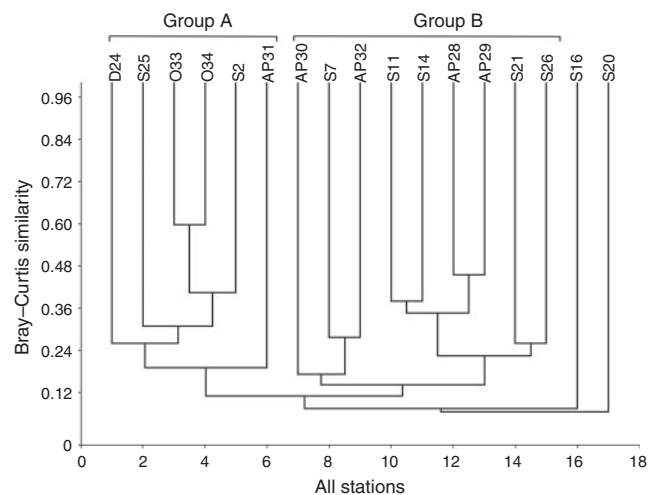


Fig. 2. Dendrogram based on taxa composition, obtained by cluster analysis using the Bray–Curtis coefficient, revealing the presence of two groups, A and B, with six and nine stations respectively.

Cluster analysis (Fig. 2) showed the presence of two major groups of sites at a similarity level of 5%: Group A with six stations (156.5–244-m depth) and Group B with nine stations (88–754-m depth). Group B is divided into three stations with considerable differences in depth (Stations AP30, AP32 and S7) and several stations from the Shetland Islands and Bransfield Strait.

ANOSIM revealed that there were significant differences in assemblages between Groups A and B (ANOSIM, global $R = 0.51$, $P = 0.001$).

Results of SIMPER for the dissimilarity between groups are given in Table 4. The bivalves *N. inaequisculpta*, *Y. eightsi* and *Lissarca notorcadensis* contributed considerably to the similarity between the stations in Group A, whereas *Pseudokellia cardiformis* contributed to the similarity between the stations in Group B. The species that contributed most to the

dissimilarity between the two groups were *N. inaequisculpta* and *Y. eightsi*, with an accumulated value of 20.63%.

Figs 3 and 4 show the dendrograms obtained on the basis of bivalves and gastropods, when they were treated separately. When considering bivalves only (Fig. 3), stations clustered into two distinct major groups; however, in the case of gastropods (Fig. 4), the separation into groups was more diffuse. In the first cluster, the bivalves that contributed most to the dissimilarity between the two groups were the nuculids *N. inaequisculpta* and *Y. eightsi*.

Feeding mode and relationships between biotic and environmental variables

The feeding ecology of molluscs varied between the 17 stations (Table 5). In several stations (S7, S11, S16, S25, AP28, AP29

Table 4. Results of SIMPER analysis (overall average dissimilarity: 90.55)
Taxa (the first 20) ranked according to their average contribution to dissimilarity between two main groups of stations

Taxa	Contribution	Cumulative percentage	Mean abundance A	Mean abundance B
<i>Nuculana inaequisculpta</i> (Lamy, 1906)	15.96	15.96	14.8	0.27
<i>Yoldia eightsi</i> (Couthouy in Jay, 1839)	4.66	20.63	4	0.36
<i>Lissarca notorcadensis</i> Melvill & Standen, 1907	4.37	25	2.67	2.36
<i>Siphonodentalium dalli</i> (Pilsbry & Sharp, 1898)	4.18	29.18	3.5	1.18
<i>Philobrya sublaevis</i> Pelseener, 1903	2.89	32.07	1.5	2.55
<i>Limopsis lilliei</i> Smith, 1915	2.53	34.6	2	0.36
<i>Pseudamauropsis aureolutea</i> (Strebel, 1908)	2.49	37.09	0.5	2.55
<i>Pseudokellia cardiformis</i> (Smith, 1885)	2.38	39.47	0	2.91
<i>Cyclocardia astartoides</i> (Martens, 1878)	2.15	41.62	0.33	2.36
<i>Laternula elliptica</i> (King & Broderip, 1832)	2.11	43.73	2.33	0
<i>Chlanidota signeyana</i> Powell, 1951	2.02	45.75	1.33	1.91
<i>Silicula rouchi</i> Lamy, 1910	1.87	47.62	1.33	0.18
<i>Propeleda longicaudata</i> (Thiele, 1912)	1.76	49.38	0.83	1
<i>Neobuccinum eatoni</i> (Smith, 1875)	1.65	51.03	0.5	1.36
<i>Notoficula bouveti</i> (Thiele, 1912)	1.62	52.65	0.33	1.55
<i>Cuspidaria infelix</i> Thiele, 1912	1.60	54.25	0.33	1.73
<i>Belaturricula</i> sp.	1.53	55.78	0.67	1.36
<i>Calliotropis pelseeneri</i> Cernohorsky, 1977	1.44	57.22	0	1.55
<i>Cuspidaria</i> sp. 1	1.24	58.46	1	0.27
<i>Limatula pygmaea</i> (Philippi, 1845)	1.18	59.63	0	1.27

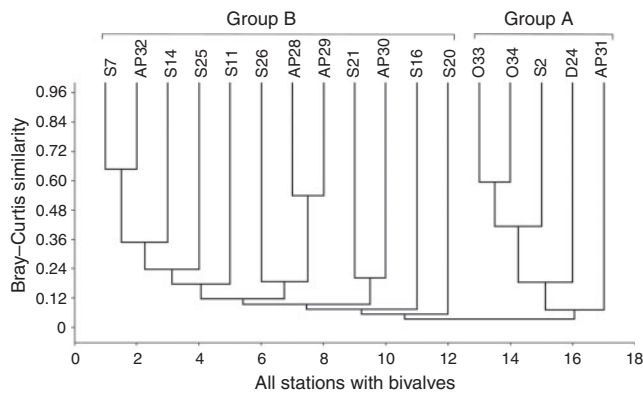


Fig. 3. Dendrogram based on bivalves, obtained by cluster analysis and using the Bray–Curtis coefficient.

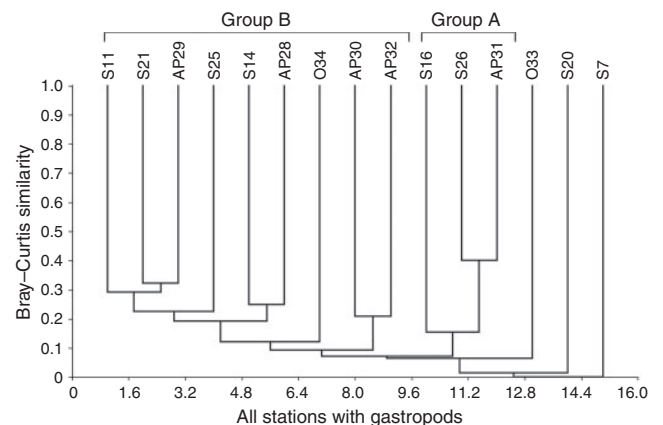


Fig. 4. Dendrogram based on gastropods, obtained by cluster analysis and using the Bray–Curtis coefficient.

and AP32), suspension feeders were the best represented group, whereas in others (S2, D24, AP31, O33 and O34) deposit feeders were best represented. Stations AP28 and S14 were the most diverse, with different proportions of five feeding habits. In Station AP28, suspension feeders (38.31%) were the best represented trophic group, followed by predators (34.83%), scavengers (17.91%), grazers (7.96%) and deposit feeders (1%). Station S14 had a higher proportion of predators (47.59%) and a slight decrease in suspension feeders relative to station AP28 (30.12%), followed by grazers (12.05%), scavengers (7.83%) and deposit feeders (2.41%). In other stations (S21 and AP30), predators were also present in similar proportions (50 and 47.83% respectively). Grazers were the best represented in only one Station (S20). Finally, Station S26 had similar proportions of suspension and deposit feeders, with values of ~30–33%.

Cluster analysis based on trophic groups (Fig. 5) showed two major assemblages, A and B. Group A includes the stations where deposit feeders dominate, whereas Group B includes two subgroups, one characterised by the dominance of suspension feeders (Subgroup B2) and the other with a higher proportion of predators (Subgroup B1).

The plot for canonical correspondence analysis (CCA) for bivalve taxa and stations, performed for the environmental data with three variables (salinity, temperature and depth), is shown in Fig. 6, with stations displayed as points and environmental variables displayed as arrows. Axis 1 is positively correlated with salinity, and negatively correlated with temperature and depth. Axis 2 is negatively correlated with depth. Sites with high and positive scores on Axis 1, such as AP28, AP29 and AP30, are characterised by high salinity and low temperatures.

Table 5. Molluscan community structure on the basis of number of specimens assembled according to feeding mode

Station	Grazers	Suspension feeders	Deposit feeders	Scavengers	Predators
S2	0.00	2.78	84.72	4.17	8.33
S7	0.00	100.00	0.00	0.00	0.00
S11	4.35	79.35	0.00	5.98	10.33
S14	12.05	30.12	2.41	7.83	47.59
S16	22.22	38.89	0.00	16.67	22.22
S20	50.67	40.00	0.00	1.33	8.00
S21	3.13	9.38	3.13	34.38	50.00
D24	0.00	9.76	90.24	0.00	0.00
S25	0.00	69.07	15.46	4.12	11.34
S26	3.33	33.33	30.00	16.67	16.67
AP28	7.96	38.31	1.00	17.91	34.83
AP29	16.39	55.74	0.00	13.11	14.75
AP30	26.09	26.09	0.00	0.00	47.83
AP31	0.00	17.24	72.41	6.90	3.45
AP32	17.24	62.07	0.00	6.90	13.79
O33	0.00	8.46	84.62	0.77	6.15
O34	0.00	16.67	52.38	3.57	27.38

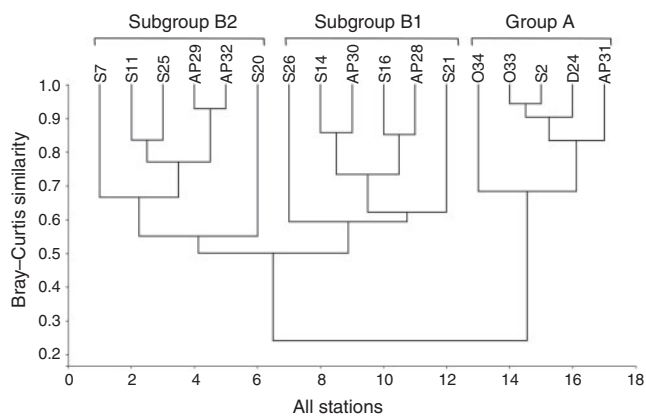


Fig. 5. Dendrogram based on trophic groups, obtained by cluster analysis using the Bray–Curtis coefficient, revealing two major assemblages, Groups A and B, with Group B divided into two subgroups, B1 and B2.

Conversely, sites O33 and D24, with high and positive scores on Axis 2, are characterised by high temperatures and low depths. Sites like S20 and S11, located towards the origin of the axis, are not affected by the environmental data or are restricted to intermediate values for the physical factors.

Convex hulls clearly separate stations from the Antarctic Peninsula and South Shetland Islands with minimal overlap between both areas along Axis 1.

Similarly, CCA for gastropod taxa and stations, performed for the environmental data with three variables (salinity, temperature and depth) is shown in Fig. 7. Axis 1 is positively correlated with salinity and negatively correlated with temperature and depth. Axis 2 is positively correlated with depth and salinity. Site AP32 shows high and positive scores on Axis 2, and is characterised by high depths and low temperatures. Conversely, sites on the extremes of Axis 1, such as S26 and

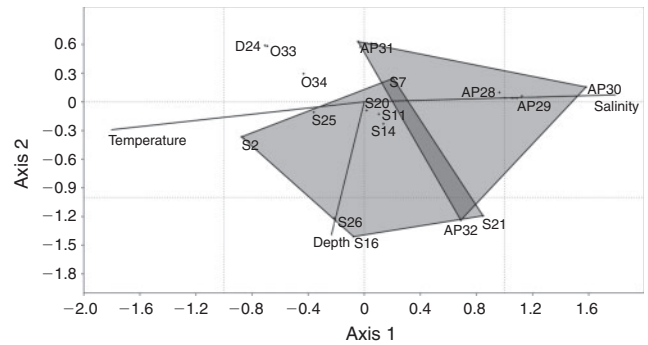


Fig. 6. Canonical correspondence analysis ordination diagram for bivalve taxa: stations are shown as points and environmental variables are shown as lines. Species are treated as points, but are not shown in the graph. Convex hulls differentiate between stations from the Antarctic Peninsula and South Shetland Islands along Axis 1.

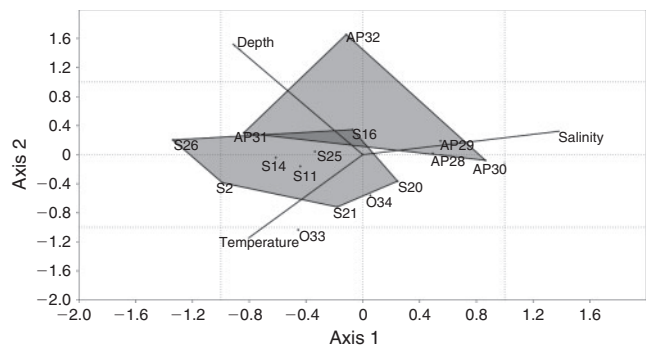


Fig. 7. Canonical correspondence analysis ordination diagram for gastropod taxa: stations are shown as points and environmental variables are shown as lines. Species are treated as points, but are not shown in the graph. Convex hulls differentiate between stations from the Antarctic Peninsula and South Shetland Islands along Axis 2. Stations S7 and D24 did not have gastropods.

AP30 (with negative and positive scores respectively), represent the small salinity gradient along the study area. Sites like S16, located towards the origin of the axis, are not affected by the environmental data or are restricted to intermediate values for the physical factors.

Convex hulls clearly separate stations from the Antarctic Peninsula and South Shetland Islands with minimal overlap between both areas along Axis 2.

Because bivalves and gastropods were considered separately in the CCA, the environmental factor structuring each group was different (Table 6). The main environmental factor structuring bivalves (along the first axis) was temperature, whereas for gastropods it was depth (along the second axis).

Size frequency distribution of two abundant nuculids

The mollusc species that most contribute to the dissimilarity between groups are the nuculids *N. inaequisculpta* and *Y. eightsi*. The range of shell length for *N. inaequisculpta* ($N = 447$) was 2.3–16.6 mm, with a higher frequency of individuals between 8 and 9.5 mm (Fig. 8). The mean (\pm s.d.) values

Table 6. Interset correlations of the canonical correspondence analysis for the bivalve assemblages and environmental factors and the gastropod assemblages and environmental factors

Bold values indicate the highest loadings associated to each axis.

	Axis 1	Axis 2
Bivalve assemblages and environmental factors		
Depth	-0.0751	-0.4900
Temperature	-0.6118	-0.1008
Salinity	0.6087	<0.001
Eigenvalue	0.27627	0.11187
Gastropod assemblages and environmental factors		
Depth	0.458823	0.763084
Temperature	0.403226	-0.574819
Salinity	0.693314	0.16155
Eigenvalue	0.246	0.16063

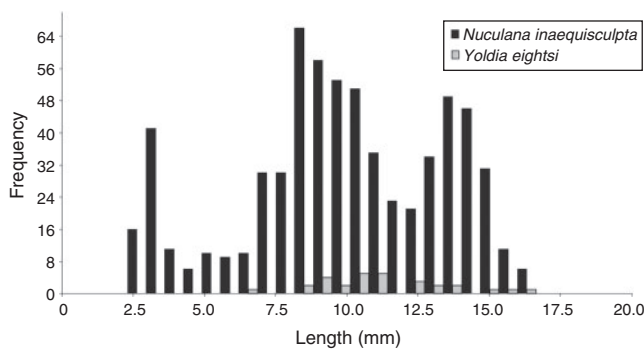


Fig. 8. Size–frequency distributions of the bivalve molluscs *Nuculana inaequisculpta* and *Yoldia eightsi* from Station D24, Deception Island, Antarctica.

of shell length, height and width were 9.9 ± 3.5 , 6 ± 2 and 4.0 ± 1.4 mm respectively. In the case of *Y. eightsi* ($N = 32$), the range of shell length was 6.8–16.7 mm, with a higher frequency of individuals of 9.5 and 11.5 mm. Mean shell length, height and width were 12.8 ± 5.4 , 8.5 ± 3.4 and 2.9 ± 1.2 mm respectively.

The Kolmogorov–Smirnov two-sample test results ($D = 0.492$, $P < 0.05$) shows that the two distributions are significantly different.

Discussion

In the present study we considered 17 mollusc assemblages collected within the West Antarctic region during the 2011 summer expedition on board RV ARA *Puerto Deseado*. Most of these correspond to the continental shelf zone, with 11 stations between 150 and 250 m, four stations at shallower locations and the remaining two deeper, between 450 and 750 m.

Consistent with previous studies in neighbouring areas in Antarctica (see Arnaud *et al.* 2001; Aldea *et al.* 2008), a common feature was that bivalves were more abundant than gastropods, but with lower species richness.

These assemblages were functionally diverse and showed considerable variation in taxa composition and diversity. At one end there are stations with high species richness values

(e.g. AP28 with 43 species) and representatives from different trophic groups, including suspension feeders, grazers, scavengers, predators and deposit feeders, whereas at the other end there is maximal abundance of only one species (*N. inaequisculpta*) and the lowest values of richness, diversity and evenness (i.e. D24). The causes of these differences are likely to be complex, although previous studies in Antarctica have pointed out that benthic assemblages are controlled by three major factors: food supply, temperature and sediment regime (Brey and Clarke 1993; Lovell and Trego 2003; Aldea *et al.* 2008). In this respect, because the latter station (D24) is located within the caldera of Deception Island, the very low species richness and dominance of deposit feeder bivalves may be attributed to strong disturbances due to recent volcanic activity, extreme sedimentation and temperature regimes. Such local geothermal activity has been shown to cause benthic and pelagic organisms to accumulate metals in their tissue, thus suppressing the success of suspension feeding fauna and inhibiting the recruitment of organisms from outer waters to the mid-bay (Deheyn *et al.* 2005).

The species *N. inaequisculpta* and *Y. eightsi* have a circum-antarctic distribution. *N. inaequisculpta* has been reported in South Orkney and the South Shetland Islands, whereas *Y. eightsi* was found in South Georgia, South Sandwich, South Orkney, South Shetland Islands and the Antarctic Weddell sector (Zelaya 2005). Particularly for Deception Island, other authors have also reported these species and similar patterns of abundance.

For example, Arnaud *et al.* (2001) observed *N. inaequisculpta* (as *Yoldiella inaequisculpta*) and *Y. eightsi* as constant species in shallow-water stations (108–170 m) at Deception Island. Lovell and Trego (2003) also found large numbers of *N. inaequisculpta* (and occasional *Laternula elliptica*) in the same area, which are main contributors to bivalve abundance and biomass. Continuing with Station D24, the size–frequency distribution calculated for the two most common species, *N. inaequisculpta* and *Y. eightsi*, showed a lower proportion of smaller individuals. This pattern may be due to a variety of factors; for example, it may be a response to a physically unstable sediment–water interface zone (formed by the burrowing and faecal pellet formation activities of the deposit feeder organisms) that provides an unstable and turbid medium offering poor support for juveniles, but not for adults (Rhoads and Young 1970). Alternatively, the scarcity or lack of young individuals may be due to predation pressure; for example, Fratt and Dearborn (1984) reported the presence of juvenile individuals of *Y. eightsi* in the stomach contents of the brittle star *Ophionotus victoriae*, a dominant ophiuroid and the main benthic biomass contributor in this site (Deception Island).

Although Station D24 differs from the rest due to its particular conditions of volcanic activity, it does conform, together with other stations (S2, AP31, O33 and O34), to a well-defined group characterised by low diversity, low depth, dominance of deposit feeders and scarcity of suspension feeders. This group is notably different from the others where suspensivorous or other trophic groups dominate. For instance, Subgroup B1 (S14, S16, S21, S26, AP28 and AP30) showed high diversity, intermediate depth values and a dominance of predators, whereas Subgroup B2 (S7, S11, S20, S25, AP29 and AP32) was defined by intermediate diversity values, high depth and dominance of suspension feeders.

These three scenarios suggest that different physical factors (e.g. topography, hydrodynamic conditions, sediment type and ice scour) may affect benthic organisms by conditioning a habitat that inhibits the development of suspensivorous groups.

Additionally, the variation of bivalves and gastropods treated separately over stations showed that bivalves were more sensitive to temperature, whereas gastropods were more sensitive to depth. Sites from the Antarctic Peninsula and South Shetland Islands were clearly differentiated, and stations closer to each other were more similar in community composition. These results were supported by CCA in relation to three environmental variables (salinity, temperature and depth). This idea is reinforced because Antarctic bivalves can generally only survive at low temperatures, and within small temperature ranges, because they are highly stenothermal (Peck and Conway 2000). It has also been found that most gastropods showed discrete depth distribution, whereas most bivalves showed broader depth ranges (Aldea *et al.* 2008). The causes of bathymetric zonation have been related primarily to physical changes (tolerance to temperature, pressure and sediment type) or biological interactions (larval dispersal, competition, predation and trophic level). The role of controlling these factors is complex and often there are no clear reasons for these patterns. However, the degree of zonation increases with trophic level or size, so faunal replacement with depth is more rapid among predators (i.e. many species of gastropods in the present study) than among infaunal or epifaunal deposit or suspension feeders, such as bivalves (Aldea *et al.* 2008).

Despite this complexity, the results of the present study, added to previous work, show evidence of differences between bivalves and gastropods with regard to limiting factors, as well as different trophic assemblages, most probably linked to the sedimentary matrix where these communities settle.

This should be taken into account when considering the effects on benthic fauna associated with climatic change and global warming. In this regard, the Antarctic Peninsula is one of the three places on Earth that has registered the most intense warming in the past 50 years and, rather than temperature, sedimentation processes will be increasing under the current scenario of glacial retreat, and attention needs to be paid to its effects along the Antarctic Peninsula (Sahade *et al.* 2015).

Therefore, it is important to continue periodic checking of faunal composition and trophic structure in these benthic Antarctic communities.

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Appendix 1. List of molluscs

The identification and taxonomic position of mollusc taxa was made following different works (Dell 1972, 1990; Absher and Feijó 1998; Linse 2002; Aldea and Troncoso 2010) and using different databases, such as the Southern Ocean Mollusc Database (SOMBASE; Griffiths et al. 2003), Malacolog, ver. 4.1.1. (G. Rosenberg, see <http://www.malacolog.org/>, accessed December 2016), the database of Antarctic and Subantarctic Marine Invertebrates provided by the National Museum of Natural History, Smithsonian Institution (R. Lemaitre, M. G. Harasewych and J. Hammock, see <http://invertebrates.si.edu/ANTIZ>, accessed December 2016) and Encyclopedia of Life (available from <http://www.eol.org>, accessed December 2016)

Class Gasteropoda	<i>Lusitromina abyssorum</i> (Lus, 1993)
Subclass Eogastropoda	<i>Neobuccinum eatoni</i> (Smith, 1875)
Order Patellogastropoda	<i>Notoficula bouveti</i> (Thiele, 1912)
Family NACELLIDAE Thiele, 1891	<i>Pareuthria regulus</i> (Watson, 1882)
<i>Nacella polaris concinna</i> (Strebel, 1908)	<i>Pareuthria</i> sp.
Family LEPETIDAE Dall, 1869	<i>Prosipho hedleyi</i> Powell, 1958
<i>Iothia coppingeri</i> (Smith, 1881)	<i>Prosipho chordatus</i> (Strebel, 1908)
Family FISSURELLIDAE	<i>Prosipho</i> sp. 1
<i>Puncturella spirigera</i> Thiele, 1912	<i>Prosipho</i> sp. 2
Subclass Orthogastropoda	Buccinidae sp. 1
Superorder Vetigastropoda	Family CANCELLARIDAE Forbes & Hanley, 1853
Family TROCHIDAE Rafinesque, 1815	<i>Nothoadmete consobrina</i> (Powell, 1951)
<i>Calliotropis pelseeneeri</i> Cernohorsky, 1977	<i>Nothoadmete antactica</i> (Strebel, 1908)
<i>Calliotropis antarctica</i> Dell, 1990	Cancellaridae sp.1
<i>Antimargarita smithiana</i> (Hedley, 1916)	Family VOLUTOMITRIDAE
Trochidae sp. 1	<i>Paradmete</i> sp. 1
Trochidae sp. 2	<i>Paradmete</i> sp.2
Trochidae sp. 3	Family VOLUTIDAE Rafinesque, 1815
Trochidae sp. 4	<i>Harpovoluta charcoti</i> (Lamy, 1910)
Trochidae sp. 5	Family CONIDAE Rafinesque, 1815
Trochidae sp. 6	<i>Belaturriculata gaini</i> (Lamy, 1910)
Trochidae sp. 7	<i>Belaturricula turrita multispiralis</i> Dell, 1990
Trochidae sp. 8	<i>Belaturricula turrita</i> (Strebel, 1908)
Trochidae sp. 9	<i>Belaturricula</i> sp.
Family TURBINIDAE	Conidae sp. 1
<i>Leptocollonia innocens</i> (Thiele, 1912)	Conidae sp. 2
Superorder Caenogastropoda	Family TURRIDAE Swainson, 1840
Family EATONIELLIDAE	<i>Aforia magnifica</i> (Strebel, 1908)
<i>Eatoniella</i> sp.	<i>Aforia multispiralis</i> Dell, 1990
Family CAPULIDAE	<i>Pleurotomella simillina</i> Thiele, 1912
<i>Torellia insignis</i> (Smith, 1915)	<i>Pleurotomella frigida</i> Thiele, 1912
<i>Torellia mirabilis</i> (Smith, 1907)	<i>Pleurotomella</i> sp. 1
<i>Torellia planispira</i> (Smith, 1915)	<i>Pleurotomella</i> sp. 2
<i>Torellia</i> sp.	<i>Conorbela antarctica</i> (Strebel, 1908)
Family NATICIDAE Forbes, 1838	<i>Leucosyrinx paratenoceras</i> Powell, 1951
<i>Pseudamauropsis anderssoni</i> (Strebel, 1906)	Turridae sp. 1.
<i>Pseudamauropsis aureolutea</i> (Strebel, 1908)	Turridae sp. 2
Naticidae sp. 1	Turridae sp. 3
Naticidae sp. 2	Superorder Heterobranchia
Naticidae sp. 3	Order Ophistobranchia
Naticidae sp. 4	Family ACTEONIDAE d'Orbigny, 1842
Family TROCHACLIDAE	<i>Neactaeonina edentula</i> (Watson, 1883)
<i>Trochaclis antarctica</i> Thiele, 1912	Family PHILINIDAE
Family CERTITHIOPSIDAE	<i>Philine</i> sp. 1
<i>Cerithiopsilla antarctica</i> (Smith, 1907)	<i>Philine</i> sp. 2
<i>Cerithiopsilla</i> sp. 1	<i>Philine</i> sp. 3
<i>Cerithiopsilla</i> sp. 2	Gasteropoda Indet
Family MURICIDAE Rafinesque, 1815	Class Bivalvia
<i>Trophon coulmanensis</i> Smith, 1907	Subclass Protobranchia
<i>Trophon</i> sp.	Order Nuculida
Muricidae sp. 1	Family NUCULANIDAE Adams & Adams, 1858
Family BUCCINIDAE Rafinesque, 1815	<i>Propeleda longicaudata</i> (Thiele, 1912)
<i>Chlanidota signeyana</i> Powell, 1951	<i>Nuculana inaequisculpta</i> (Lamy, 1906)
<i>Chlanidota</i> sp.	

(Continued)

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- Family YOLDIIDAE Habe, 1977
Yoldia eightsi (Couthouy in Jay, 1839)
- Family SILICULIDAE Allen & Sanders, 1973
Silicula roochi Lamy, 1910
- Subclass Pteriomorpha
Order Arcida
Family ARCIDAE
Bathyarca sinuata Pelseneer, 1903
- Family LIMOPSIDAE Dall, 1895
Limopsis enderbyensis Powell, 1958
Limopsis lilliei Smith, 1915
Limopsis marionensis Smith, 1885
Limopsis sp.
- Family PHILOBRYIDAE Bernard, 1897
Lissarca notorcadensis Melvill & Standen, 1907
Philobrya sublaevis Pelseneer, 1903
- Order Mytilida
Family MYTILIDAE Rafinesque, 1815
Dacrydium albidum Pelseneer, 1903
- Order Limida
Family LIMIDAE Rafinesque, 1815
Limatula pygmaea (Philippi, 1845)
Limatula hodgsoni (Smith, 1907)
Limatula simillima Thiele, 1912
- Subclass Heterodonta
Order Venerida
Family THYASIRIDAE Dall, 1901
Thyasira sp.
- Family CARDITIDAE Fleming, 1828
Cyclocardia astartoides (Martens, 1878)
- Family GALEOMMATIDAE
Mysella sp.
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- Family CYAMIIDAE Philippi, 1845
Cyamiomacra laminifera (Lamy, 1906)
Cyamiocardium denticulatum (Smith, 1907)
Pseudokellia cardiformis (Smith, 1885)
- Subclass Anomalodesmata
Order Pholadomyida
Family LYONSIIDAE Fischer, 1887
Lyonsia arcaeformis Martens, 1885
- Family POROMYIDAE
Poromya adelaidis (Hedley, 1916)
- Family LATERNULIDAE Hedley, 1918
Laternula elliptica (King & Broderip, 1832)
- Family THRACIIDAE Stoliczka, 1870
Thracia meridionalis Smith, 1885
- Family CUSPIDARIIDAE Dall, 1886
Cuspidaria infelix Thiele, 1912
Cuspidaria sp. 1
Cuspidaria sp. 2
Bivalvia Indet sp. 1
Bivalvia Indet sp. 2
Bivalvia Indet sp. 3
- Class Scaphopoda
Order Dentaliida
Family DENTALIIDAE
Dentalium majorinum Mabilie & Rochebrune, 1889
- Family GADILIDAE Stoliczka, 1868
Siphonodentalium dalli (Pilsbry & Sharp, 1898)
- Class Polyplacophora
Order Neoloricata
Family ISCHNOCHITONIDAE Dall, 1889
Nuttalochiton mirandus (Thiele, 1906)
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