

Macrobenthic mollusc fauna inhabiting *Halopteris* spp. subtidal fronds in São Miguel Island, Azores*

ANA CRISTINA COSTA and SÉRGIO PAULO ÁVILA

Departamento de Biologia, Universidade dos Açores, Rua da Mãe de Deus, 9500 Ponta Delgada.
E-mail: costa@alf.uac.pt, avila@alf.uac.pt

SUMMARY: The molluscan community structure (species composition, abundance, density and diversity) associated with common brown algae *Halopteris* spp. at seven subtidal sites on São Miguel island (Azores) was studied and checked for differences between sites. A total of 8,921 specimens (29 species of Gastropoda, 7 species of Bivalvia) were recorded. *Bittium* sp., the most common species, representing 85.6% of the total number of molluscs sampled, was present at each site and the number of taxa found at each station ranged from 3 to 17. Four species (*Bittium* sp., *Setia subvaricosa*, *Tricolia pullus azorica* and *Rissoa guernei*) accounted for 96.6% of all the specimens sampled. The density of the molluscs reached 18,000 specimens/100 g of algal dry weight (ADW). No significant differences in species diversity were found between sites. Further multispecies analysis between sites were conducted with both clustering and ordination techniques, and showed some separation between samples from south and north locations. The species responsible for this separation were the endemic Azorean Rissoids *Rissoa guernei* and *Setia subvaricosa*.

Key words: Mollusca, *Halopteris*, biological association, Azores.

INTRODUCTION

In the Azores, studies on marine molluscs inhabiting shallow-waters were mainly taxonomic until Chapman (1955) carried out the first ecological approach. Other works with a similar perspective were those by Morton (1967), Martins (1980), Arruda and Gordo (1984), Lemos and Viegas (1987), Bullock *et al.* (1990), Hawkins *et al.* (1990), Neto and Azevedo (1990), Azevedo (1991, 1992), Bullock (1995) and Ávila (1996, 1998).

In the intertidal algal turf of S. Miguel, mollusc abundance and diversity are related to the algal composition of the turf (Azevedo, 1991). It is therefore important to investigate the particular assemblage

associated with each species of algae. In the very heterogeneous rocky bottom characteristic of the Azores, the confounding factor of different compositions of algal turf must be taken into account when faunal assemblages from different places are compared. Thus, when the aim is to study the biological associations between molluscs and algae in the Azores, a different method to the traditional scraping area is necessary.

Along the shores of São Miguel, brown algae (*Halopteris filicina* and *Stylocaulon scoparium*, formerly *Halopteris scoparia*) are common. At a 15 m water depth, *S. scoparium* is one of the dominant algal species throughout the year (Neto, 1997). The abundance and distribution of these algal species make them a general representative habitat for macrobenthic subtidal communities in the Azores (Neto *et al.*, 2000).

*Received March 29, 1999. Accepted November 18, 2000.

The main objectives of this work were to characterise the molluscan fauna associated with *Halopteris* spp., to relate spatial differences in molluscan assemblages to different environmental conditions and to determine whether molluscs were potential indicators of environmental pollution.

MATERIALS AND METHODS

Samples were taken from 7 sites on São Miguel ($37^{\circ}42'N$ to $37^{\circ}55'N$ and $25^{\circ}08'W$ to $25^{\circ}52'W$), the largest island of the archipelago (Fig. 1). Sites were chosen with different environmental conditions such as location (north/south), degree of exposure (exposed/sheltered) and degree of disturbance (not-polluted/polluted/disturbed). Ribeira Quente (RQ) was classified as a naturally disturbed site, because of the existence of a shallow-water subtidal vent there. Plants were collected near the vents, limiting the depth of collection of *Halopteris* spp. at this site (Table 1). Polluted sites were those located near factory outlets, e.g. Atalhada (ATA) and Cofaco (COF). Effluents from food and fish processing factories are discharged directly onto the shore, less than 100 m from the sampling points. As there are no available data on the composition of these effluents, the degree of disturbance was estimated.

As far as possible, the sites were standardized for depth (measured using a depth gauge) and to avoid seasonal effects all samples were taken within 4 weeks in October/November 1996 (Table 1). At each site, three replicates of ten plants of *Halopteris* spp. (*Halopteris filicina* and *Stylocaulon scoparium*) were taken by diving; the sampling area was located using a two digit random method adapted from Fenwick (1984). On arrival at the bottom, a transparent disk with 10 numbered lines (0-9) was put over the compass so that the 0 would be aligned with the N direction. The first random digit indicated a direction corresponding to a radial line and the second digit determined the distance from the initial position in metres along a graduated line. At each location ten plants were gently pulled off the rock by hand and put in a labeled cotton drawstring bag. In the laboratory, the samples were washed several times and the animals were removed by pouring the washing water through a 0.5 mm mesh sieve. The samples were labeled and preserved in 70% ethanol. After draining for about 30 min, the wet weight of the algae was determined (± 0.01 g). The algae were then dried for 48 h at 60°C , and re-weighted (± 0.01

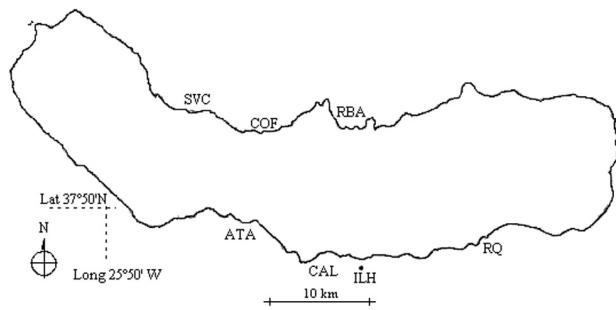


FIG. 1. – São Miguel island with the sampling sites: ATA - Atalhada; CAL - Caloura; COF - Cofaco; ILH - Vila Franca islet; RQ - Ribeira Quente; RBA - Ribeirinha; SVC - São Vicente.

g.). This allowed the faunal results to be standardized avoiding any bias resulting from different sized plants. *Halopteris filicina* and *Stylocaulon scoparium* are larger on the north coast than in the south coast of S. Miguel (Neto, 1997). The samples were sorted under a binocular dissecting microscope and separated into major groups (Polychaeta, Mollusca, Crustacea, Ophiuroidea, others). The molluscs were sorted into species and counted.

Data analysis

Data analysis was undertaken using the PRIMER (Plymouth Routines in Multivariate Ecological Research) set of programs developed and tested by Plymouth Marine Laboratory, and by MINITAB Release11 statistical package.

TABLE 1. – Characterisation of the samples collected in 1996.

	Date (1996)	North/ South coast	Water temperature (°C)	Depth (m)	Wet weight (g)	Dry weight (g)
ATA1	10-Oct	S	21	11.2	18.91	4.61
ATA2	10-Oct	S	21	11.2	11.76	2.47
ATA3	10-Oct	S	21	11.2	17.49	4.21
CAL1	14-Oct	S	21	13.7	11.54	6.24
CAL2	14-Oct	S	21	13.7	14.09	3.70
CAL3	14-Oct	S	21	13.7	20.84	5.79
COF1	05-Nov	N	20	11.3	75.98	13.26
COF2	05-Nov	N	20	11.3	107.01	17.48
COF3	05-Nov	N	20	11.3	13.57	8.83
ILH1	24-Oct	S	20	15.0	1.87	0.38
ILH2	24-Oct	S	20	15.0	8.59	1.81
ILH3	24-Oct	S	20	15.0	1.85	0.41
RBA1	08-Oct	N	21	12.2	96.30	21.89
RBA2	08-Oct	N	21	12.2	18.86	4.59
RBA3	08-Oct	N	21	12.2	31.25	5.91
RQ1	15-Oct	S	21	5.5	82.75	19.49
RQ2	15-Oct	S	21	5.5	59.25	16.20
RQ3	15-Oct	S	21	5.5	47.47	13.28
SVC1	07-Oct	N	21	11.0	39.08	6.80
SVC2	07-Oct	N	21	11.0	32.67	6.38
SVC3	07-Oct	N	21	11.0	37.94	5.78

Other abbreviations as in Figure 1.

Mollusc density, defined as the total number of specimens of a species (n_i) per 100 g of algal wet weight ($n_i/100$ g AWW) or algal dry weight ($n_i/100$ g ADW), was calculated. Correlations (Pearson coefficient) between total abundance (N/100 g ADW) and ADW were also calculated, N being the total number of molluscs per sample.

Species diversity was measured using several indices: Species richness (S), species diversity indices of Margalef (D) (DoCampo and Bikuna, 1994; Schoch and Dethier, 1996), Shannon-Wiener (H') (Fenwick, 1976; Pearson and Rosenberg, 1978; Pité and Avelar, 1996) and Pielou (J') (Pearson and

Rosenberg, 1978; Warwick and Clarke, 1993a), Simpson's dominance index (Si) (Carr, 1996) and total number of molluscs per sample (N).

ANOVA was performed to identify diversity differences between sites. At the sites where significant differences were found, Hsu's MCB test (Multiple Comparisons with the Best, family error rate = 0.05, Minitab, 1996) was performed to identify the sites responsible for the differences.

To determine whether there were relationships between algal biomass and associated malacofauna, Pearson's correlation coefficient (r) was calculated using the abundance (N/100 g ADW) and

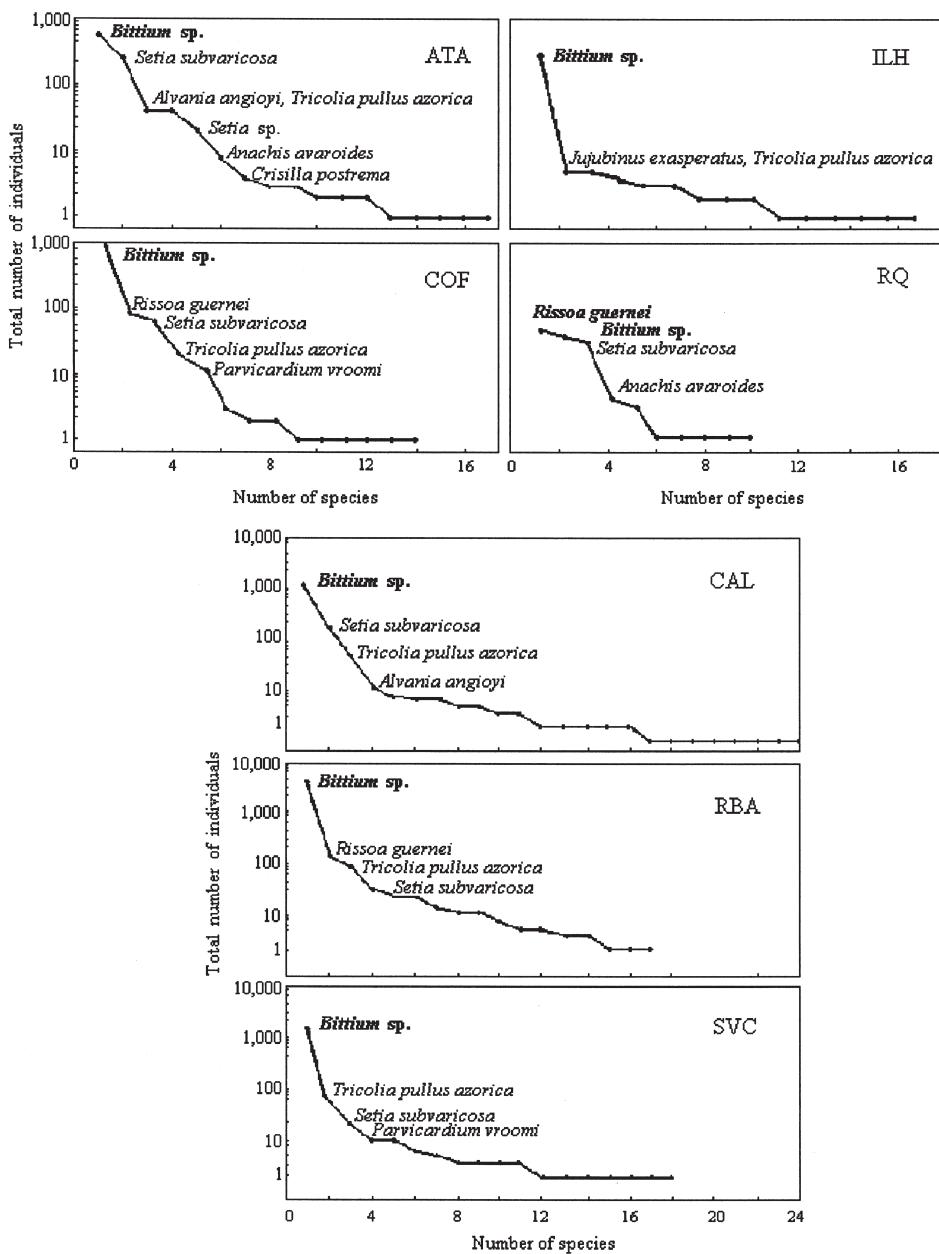


FIG. 2. – Rank abundance curves (total number of individuals) for the molluscan species collected at each site. Other abbreviations as in Figure 1.

diversity indices that had been determined. In addition to univariate analysis, multispecies analysis between sites was conducted with ordination techniques. Prior to the multivariate analysis, actual numbers ($n/100$ g ADW) were transformed by double square root transformation to standardise the data and to ensure that the multivariate ordination was not determined by the most abundant species (Clarke *et al.*, 1993).

Transformed species abundance [$(n/100$ g ADW) $^{1/4}$] and Shannon diversity data were used to generate triangular matrices of similarities, using the Bray-Curtis coefficient (Bray Curtis, 1957 *fide* Gray *et al.*, 1988). Similarity matrices were subjected to clustering and ordination analysis (multidimensional scaling ordination – MDS) (Warwick *et al.*, 1990). Clustering was done by the hierarchical agglomerative method employing group-average linking (UPGMA).

The ANOSIM randomization/permutation test (Warwick and Clarke, 1993a) was used to test for differences between sites or selected sets of sites. Species with a ratio higher than 1.4 (SIMPER analysis) were considered as mainly responsible for the dissimilarity between places/sites (Warwick *et al.*, 1990).

RESULTS

Of the total of 8,921 specimens, there were 36 species (29 species of Gastropoda and 7 of Bivalvia) belonging to 19 families (14 Gastropoda and 5 Bivalvia). Rissoidae was the best represented family, with 9 species. *Bittium* sp., a species endemic to the Azores and not yet described, *Setia subvaricosa*, *Tricolia pullus azorica* and *Anachis avarooides* were present in all samples, whereas *Alvania poucheti*, *Alvania sleursi*, *Odostomella doliolum*, *Arca tetragona*, *Cerithiopsis barleei*, *Eulima* sp. and *Plagiocardium papillosum* were found only once, the first three at CAL. *Bittium* sp. was present at each site and formed 85.6% of the total number of molluscs sampled. Four species (*Bittium* sp., *S. subvaricosa*, *T. pullus azorica* and *Rissoa guernei*) accounted for 96.6% of all specimens sampled (Fig. 2). Ribeirinha (RBA) was the site with the highest number of molluscs, with a total of 3,882 animals. At RQ and Ilhéu de Vila Franca (ILH), only 118 and 406 specimens were found respectively.

Once the biomass values for the algae (wet and dry weight) were known, a regression was calculat-

TABLE 2. – Correlation coefficient (Pearson) between abundance of molluscs (N/100 g ADW) and algal dry weight (ADW) for each sampling site. Other abbreviations as in Figure 1.

	r
ATA	0.638
CAL	-0.997
COF	-0.940
ILH	0.680
RBA	0.007
RQ	-0.999
SVC	0.832

TABLE 3. – Species richness (S), total number of molluscs per site (n), diversity indices of Margalef (D), Shannon-Wiener (H') and Pielou (J'), Simpson's dominance index (Si). Other abbreviations as in Figure 1.

	S	n	D	H'	J'	Si
ATA1	15	339	2.400	1.370	0.506	0.350
ATA2	9	124	1.660	1.180	0.537	0.389
ATA3	9	497	1.290	0.917	0.417	0.568
CAL1	17	399	2.670	1.020	0.359	0.537
CAL2	11	406	1.660	0.484	0.202	0.819
CAL3	16	437	2.470	0.816	0.294	0.667
COF1	8	284	1.240	0.944	0.454	0.545
COF2	10	228	1.660	1.050	0.455	0.541
COF3	6	548	0.790	0.427	0.239	0.825
ILH1	6	15	1.850	1.410	0.789	0.333
ILH2	12	329	1.900	0.363	0.146	0.883
ILH3	5	62	0.970	0.388	0.241	0.847
RBA1	15	2725	1.770	0.305	0.113	0.896
RBA2	8	794	1.050	0.373	0.179	0.856
RBA3	11	363	1.700	0.317	0.132	0.898
RQ1	4	11	1.250	1.160	0.838	0.355
RQ2	3	43	0.530	0.967	0.880	0.408
RQ3	8	64	1.680	1.470	0.706	0.277
SVC1	13	1101	1.710	0.245	0.095	0.924
SVC2	7	101	1.300	1.140	0.587	0.402
SVC3	6	51	1.270	0.987	0.551	0.459

ed: $ADW = 1.373 + 0.188AWW$ ($r^2 = 0.86$; $p < 0.05$). ILH and RBA were the sites with highest density values, respectively 12,415 and 11,963 molluscs/100 g ADW (average of the three replicates). At ILH2 more than 18,000 molluscs/100 g ADW were found (Appendix).

A very strong negative correlation was found between mollusc abundance and ADW in samples from CAL, COF and RQ. The only significant positive correlation was found at SVC, whereas at RBA the number of animals found seems to be independent from the sampled algal mass (Table 2).

The number of species per replicate ranged from 3 (RQ2) to 17 (CAL1); RQ is the site with lowest species richness, whereas the highest number of species was found at CAL. Margalef's diversity index ranged between 0.53 (RQ2) and 2.67 (CAL1). Both Shannon-Wiener's and Pielou's diversity indices reached the highest values at RQ. Pielou's

TABLE 4. – Pearson's correlation between abundance (N/100 g ADW) and diversity indices used. Other abbreviations as in Figure 1.

	S	D	H'	J'	Si
ATA	-0.177	-0.490	-0.714	-0.996	0.871
CAL	-0.996	-0.998	-0.990	-0.984	0.973
COF	-0.935	-0.942	-1.000	-0.988	0.989
ILH	0.562	-0.267	-0.983	-0.998	0.989
RBA	-0.358	-0.773	0.721	0.635	-0.849
RQ	0.763	0.380	0.619	-0.734	-0.601
SVC	0.996	1.000	-0.980	-0.994	0.990

TABLE 5. – One-way ANOVA applied on diversity indices. Abbreviations as in Table 4. F_{calc} - F-value calculated; F_{crit} - F-value critical; p - p-value. * - significant.

	F_{calc}	F_{crit}	p
D	1.819	2.850	0.167
H'	2.002	2.848	0.134
J'	3.838	2.848	0.018*
Si	2.689	2.848	0.060

diversity index had the lowest values at RBA. Simpson's dominance index had low values at RQ and ATA, reaching a maximum at SVC (Table 3).

From Pearson's correlation coefficient (r) between abundance (N/100 g ADW) and the diversity indices (Table 4), it is clear that the most diverse sites were not the ones with higher abundances, since most of the significant correlations were negative. The exception was SVC, where a strong positive correlation for S, D and Si was found (Table 4). This last index is positively correlated with abundance at all sites but RBA and RQ. Although there appears to be some variation in the values of the diversity indices among the sampling sites (Table 3), a significant difference (ANOVA) was found only for equitability values (J' index) (Table 5). The site responsible for this difference was RQ, as detected by Multiple Comparison test, Hsu's MCB (Fig. 3).

Three main groups were obtained by classification analysis at 50% similarity (Fig. 4). One consists of one sample (RQ1), the second is formed by a combination of the remaining RQ samples together with all the replicates from COF and two samples from SVC. All other samples formed the third group. Some variability was detected among the replicates within sites, except at ATA and COF, where the three samples are clustered with a high degree of similarity and before any other connection to other groups (Fig. 4).

Classification analysis over Shannon's diversity index data results in two groups. The first has all the

samples from ATA and RQ, and two samples each of SVC, CAL and COF. The second group, comprising fewer stations than the first one, has all the samples from RBA and two samples of ILH (Fig. 5).

The results of MDS ordination (Fig. 6) do not show distinct clustering except for the samples from RQ, particularly RQ1. However, there is a concentration of samples from the north shore in the left/centre of the plot while the south coast samples are shifted to the right side (RQ being the only exception). Replicates from some sites (e.g. RQ, SVC and ILH) are scattered apart and/or among other samples, reflecting great variability of their faunistic composition.

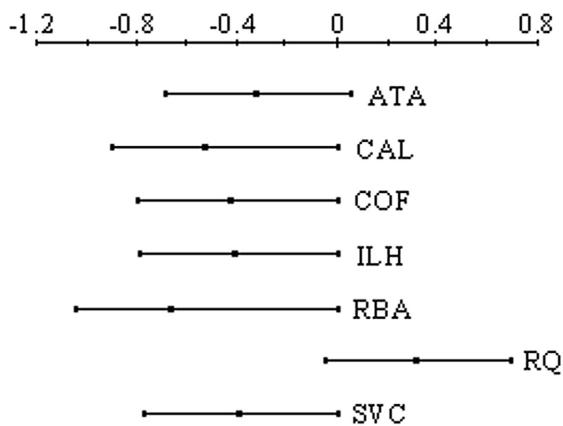


FIG. 3. – Results for the Hsu's Multiple Comparisons with the Best, in J' values.

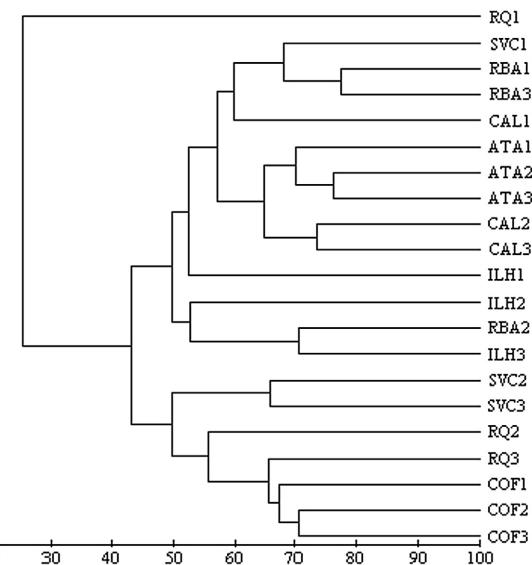


FIG. 4. – Cluster analysis of the molluscan fauna associated with *Halopteris* spp. Data transformed by the formula $y_i = (n_i/100g ADW)^{1/4}$; Bray-Curtis similarity index, UPGMA. Abbreviations as in Figure 1.

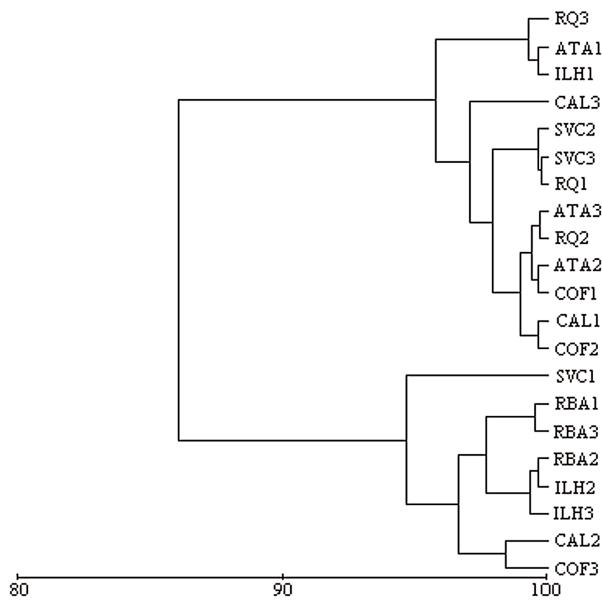


FIG. 5. – Cluster analysis of the molluscan fauna associated with *Halopteris* spp. Shannon-Wiener diversity index calculated from data transformed by the formula $y_i = (n_i/100 \text{ g ADW})^{1/4}$, Bray-Curtis similarity index, UPGMA. Abbreviations as in Figure 1.

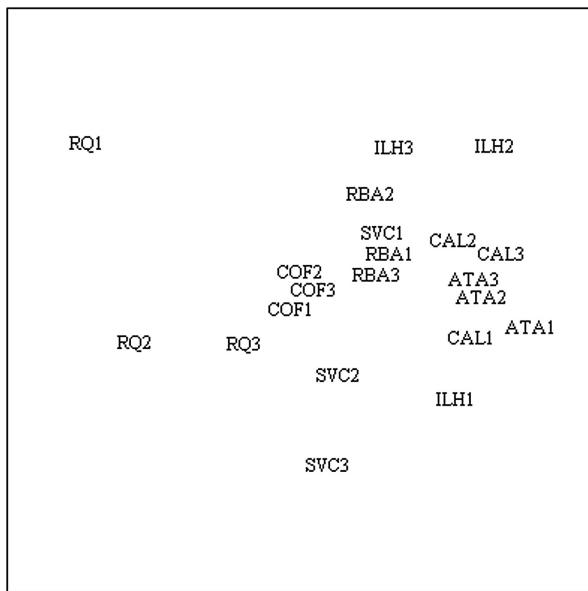


FIG. 6. – Two-dimensional MDS configuration. Stress=0,16.

TABLE 6. – Pre-defined groups and their abbreviations used in ANOSIM and SIMPER analysis. Abbreviations of the sampling sites as in Figure 1.

Pre-defined groups	Sampling sites
N - north shore	COF, RBA, SVC
S - south shore	ATA, CAL, ILH, RQ
NP - non-polluted site	CAL, ILH, RBA, SVC
D - disturbed site	RQ
P - polluted site	ATA, COF
Exp - exposed site	ATA, CAL, COF, ILH, RQ, SVC
She - sheltered site	RBA

TABLE 7. – ANOSIM results. Data transformed by the formula $y_i = (n_i/100 \text{ g ADW})^{1/4}$. Other abbreviations as in Table 6.

Group comparisons	R	Significance level (%)
N/S	0.086	11.7
NP/D/P	0.309	0.6
NP/(D+P)	0.183	1.5
Exp/She	-0.249	94.4

A total of 20,000 permutations was used (ANOSIM) to compare the pre-defined groupings of replicates (north/south sites; non-polluted/disturbed/polluted sites; exposed/sheltered sites) against random simulations (Table 6). The significance level of the test statistic R was high (94.4%) only with Exposed compared with Sheltered sites (Table 7). However, this may be related to the fact that only one sheltered site (RBA) is being compared to the heterogeneous group consisting of all other samples.

SIMPER analysis indicated that *Rissoa guernei* (Rg) and *Setia subvaricosa* (Ss) were the species responsible for the separation of north and south samples. The absence of *Tricolia pullus azorica* (Tpa) and the lower numbers of *Bittium* sp. (Bi) seem to be an important factor for discriminating RQ samples from the others. These same species, together with Ss and Rg, seem to be discriminant for distinguishing RQ from the sites considered as polluted. *Setia subvaricosa* (Ss) discriminated between non-polluted sites (NP) and other sites (D+P). The most discriminant species between sheltered (RBA) and all other sites (exposed) are *Ocinebrina aciculata* (Oa), *Rissoa guernei* (Rg) and *Setia subvaricosa* (Ss) (Table 8).

DISCUSSION

Our results confirm that Rissoidae is the best represented mollusc family associated with algae in the Azores (e.g. Azevedo, 1991; Bullock *et al.*, 1990; Gofas, 1990; Ávila, 1996, 1998). *Bittium* sp., *S. subvaricosa*, *T. pullus azorica* and *Anachis avaroides* characterise all our samples.

In Table 9, our results on species densities are compared with the results obtained by Bullock *et al.* (1990), who worked with mollusc fauna of *Stylocaulon scoparium* (quoted as *Halopteris scoparia*) from ILH, and with those of Azevedo (1991), which refer to a mixed algal substratum

TABLE 8. – SIMPER results. Data transformed by the formula $y_i = (n_i/100 \text{ g ADW})^{1/4}$. Aa: *Alvania angioyi*. An: *Anachis avaroides* Bi: *Bittium* sp. Js: *Jujubinus striatus*. Oa: *Ocinebrina aciculata*. Pv: *Parvicardium vroomi*. Rg: *Rissoa guernei*. Ss: *Setia subvaricosa*. Se: *Setia* sp. Tpa: *Tricolia pullus azorica*. Other abbreviations as in Table 6.

Groups of sites	Average similarity	Species	Species % (Ratio of each species)	Cumulative %
N	57.29	Bi - Tpa - Rg - Ss - An	39.06 - 18.49 - 16.85 - 9.80 - 4.25 (5.49 - 3.56 - 3.91 - 1.04 - 0.82)	88.45
S	43.23	Bi - Ss - Tpa - An - Aa	38.19 - 17.47 - 14.32 - 6.92 - 6.76 (2.98 - 1.30 - 1.32 - 0.81 - 0.82)	83.67
NP	52.33	Bi - Tpa - Ss - An - Rg - Aa	41.44 - 20.35 - 6.71 - 4.99 - 4.29 - 3.97 (4.61 - 3.28 - 0.80 - 0.83 - 0.65 - 0.66)	81.75
D	45.99	Bi - Ss	48.81 - 33.76 (4.22 - 4.18)	82.57
P	57.97	Bi - Ss - Tpa - An	35.97 - 22.62 - 16.51 - 6.83 (5.24 - 4.72 - 6.47 - 1.32)	81.93
D+P	46.39	Bi - Ss - Tpa - Rg	36.60 - 26.14 - 10.62 - 10.52 (3.35 - 3.71 - 1.11 - 0.60)	83.88
Exp	45.82	Bi - Tpa - Ss - Rg - An	39.72 - 17.12 - 16.42 - 5.62 - 5.15 (3.51 - 1.61 - 1.31 - 0.49 - 0.70)	84.03
She	67.55	Bi - Rg - Tpa - An - Oa	38.64 - 14.05 - 11.69 - 9.02 - 7.69 (13.17 - 7.12 - 4.82 - 12.04 - 6.03)	81.09
Groups	Average dissimilarity	Species	Species % (Ratio of each species)	Cumulative %
N/S	52.80	Bi - Rg - Ss - Aa - Tpa - Pv - An	11.40 - 8.74 - 8.26 - 5.83 - 5.64 - 5.37 - 4.98 (1.19 - 1.85 - 1.54 - 1.23 - 0.82 - 1.06 - 1.09)	50.22
NP/D	68.46	Bi - Tpa - Rg - Ss - An - Pv	19.01 - 11.63 - 6.39 - 6.22 - 5.16 - 5.12 (2.71 - 2.03 - 1.35 - 1.62 - 1.08 - 1.04)	53.52
NP/P	47.86	Ss - Bi - Rg - Aa - Pv - Se - An - Js	9.79 - 8.39 - 6.54 - 6.11 - 5.34 - 5.34 - 4.66 - 3.99 (1.44 - 1.50 - 1.28 - 1.26 - 1.12 - 1.18 - 1.14 - 0.80)	50.16
P/D	61.29	Bi - Tpa - Ss - Rg - Aa - An	17.13 - 11.21 - 10.11 - 7.36 - 6.78 - 5.70 (2.50 - 2.58 - 1.66 - 1.02 - 1.19 - 1.48)	58.30
NP/(D+P)	54.72	Bi - Ss - Tpa - Rg - Aa - Pv - An - Se	12.82 - 8.30 - 6.64 - 6.48 - 5.61 - 5.25 - 4.87 - 4.21 (1.27 - 1.48 - 0.92 - 1.28 - 1.20 - 1.06 - 1.05 - 1.04)	54.18
She/Exp	48.15	Bi - Rg - Ss - Pv - Oa - Aa	12.23 - 8.20 - 7.81 - 5.98 - 5.59 - 5.28 (1.09 - 1.57 - 1.49 - 1.14 - 1.98 - 1.24)	45.09

TABLE 9. – Maximum density of molluscs/100 g algal wet weight/dry weight in the present and previous works in the Azores.

	This work wet weight	Monospecific <i>Halopteris</i> samples Bullock <i>et al.</i> , 1990 wet weight	This work dry weight	Scrapped samples Azevedo, 1991 dry weight
<i>Alvania angioyi</i>	173 †	573	713 †	5,706
<i>Anachis avaroides</i>	108		488	
<i>Bittium</i> sp.	3,597	94	17,072	10,446
<i>Cardita calyculata</i>	54		244	212
<i>Hinnites distortus</i>	54		263	
<i>Jujubinus exasperatus</i>	12		276	
<i>Jujubinus</i> sp.	107		526	
<i>Ocinebrina aciculata</i>	35		166	30
<i>Parvicardium vroomi</i>	64 ‡		261 ‡	
<i>Rissoa guernei</i>	138 ‡	2841	566 ‡	5,744
<i>Setia subvaricosa</i>	714 †		2,928 †	
<i>Tricolia pullus azorica</i>	107	200	526	4,587

† - sample collected at ATA; ‡ - sample collected at RBA; all other samples collected at ILH.

collected subtidally at RBA by the scrapping method. The density of *Bittium* sp. found by us at ILH, is the highest ever reported in the Azores ($d=17,072$ molluscs/100 g ADW). Bullock *et al.* (1990) reported much lower densities of *Bittium* sp. in *Halopteris scoparia* at Vila Franca islet. Ávila (1996, 1998) found this species in the intertidal of a sheltered lagoon at Lajes do Pico, but

always in low densities, suggesting a preference of this species for subtidal conditions. The densities of *S. subvaricosa* (2,928 molluscs/100 g ADW) and *Alvania angioyi* (713 molluscs/100 g ADW), both at ATA, were also high. However, the densities of *A. angioyi*, *Rissoa guernei* and *T. pullus azorica* reported here for RBA are lower than those from Azevedo (1991) (Table 9).

Bittium reticulatum was also a very abundant species in samples of *Halopteris scoparia* taken by Borja (1986a) on the Basque Coast (Northern Spain), *Rissoa parva* being the dominant species. In our work, *Rissoa guernei* is found at all sites except ATA and ILH, being the most abundant species in the samples from RQ. Fernández *et al.* (1988) found very high quantities of *B. reticulatum* in the algae *Gelidium latifolium* at Bañugues in the north of Spain. As Borja (1986b) and Fernández *et al.* (1988) state that *B. reticulatum* is particularly abundant in November, our sampling period might have had some influence on the high abundance results found for the Azorean *Bittium*. However, at least in the infralittoral communities studied by Azevedo (1991), the seasonal variation in *Bittium* sp. density is not very marked in spite of the higher abundance found for the species in the winter months, especially at the more exposed sites and particularly on the north shore of São Miguel island. Working with other macroalgae species would make it possible to determine whether in the Azores, *Bittium* sp. conforms to the statement of Fretter and Graham (1981) that *B. reticulatum* is quite independent from the macrophyte habitat.

Azevedo (1992) found that a high ADW was associated with a high number of molluscs, but decreased diversity due to dominance. In our work, ADW was not related to mollusc abundance, except for SVC. However, high abundance of molluscs favoured dominance and decreased diversity at most of the sites sampled by us, *Bittium* sp. being the taxon responsible for this.

The highest diversity values were found at CAL (Margalef index), which is the richest place in species number. However, the higher dominance of *Bittium* sp. and *Setia subvaricosa* lowering equitability is reflected by the modest value for Shannon-Wiener diversity. This location was previously reported to have higher diversity in the intertidal mollusc assemblages as opposed to RBA (Azevedo, 1991).

The highest Shannon-Wiener index values for RQ are due to the fact that, although RQ is poor in both species richness and abundance, specimens were quite evenly distributed among species. ANOVA performed over the diversity values did not find any significant differences between sites, except for the equitability values, where RQ proved to be the place responsible for the detected difference. The low number of species and animals found at this spot was responsible for its separation under most of the performed analysis. Both classification

and ordination placed RQ closer to the northern than the southern sites. However, some caution is advised before any connection between these findings and the unusual features of the place, as other factors such as depth and sand proximity could act as confounding factors.

Some variability detected among replicates was also apparent both in classification and ordination analysis, especially for RQ and ILH. Warwick and Clarke (1993b) found that the variability of samples from impacted sites in a number of studies was much greater than the variability of those from control sites. However, in our analysis, the replicates from two previously considered polluted sites, COF and ATA, seemed to be very consistent (Fig. 6).

As no significant difference was found between the “polluted” and “non-polluted” sites, it appears that mollusc assemblages do not constitute a good indicator of stressed benthic communities in S. Miguel.

ACKNOWLEDGEMENTS

We gratefully acknowledge valuable comments and suggestions by Dr. Ian Tittley and Prof. Malcolm Jones, two anonymous referees and the editor of *Scientia Marina* who significantly improved the manuscript. This study was supported by a grant given to the second author by JNICT (PRAXIS XXI/BIC/2788/96).

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Scient. ed.: J.D. Ros

APPENDIX. – Molluscan abundance (n/100g ADW) of the three replicate samples at each of the sampled sites in São Miguel island, Azores. Other abbreviations as in Figure 1.

	SVC1	SVC2	SVC3	RBA1	RBA2	RBA3	ATA1	ATA2	ATA3	CAL1	CAL2	CAL3	RQ1	RQ2	RQ3	ILH1	ILH2	ILH3	COF1	COF2	COF3
<i>Alvania angioyi</i>	44	0	0	18	0	51	217	40	713	0	54	138	0	0	8	263	55	0	0	6	0
<i>Alvania cancellata</i>	0	0	0	0	0	0	0	0	0	32	0	0	0	0	0	0	0	0	0	0	0
<i>Alvania poucheti</i>	0	0	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	0	0	0	0
<i>Alvania slevensi</i>	0	0	0	0	0	0	0	0	0	0	17	0	0	0	0	0	0	0	0	0	0
<i>Anachis avarooides</i>	29	0	0	37	65	17	43	40	119	32	54	52	21	0	0	0	0	488	15	6	0
<i>Arca tetragona</i>	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Bittium</i> sp.	15,559	878	519	11,777	15,991	5,821	3,167	1,943	8,694	4519	9,919	6,114	26	105	105	2,105	17,072	13,902	1,538	944	5,629
<i>Bivalvia</i> n.id.	0	0	17	0	0	0	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cardita calyculata</i>	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0
<i>Cerithiopsis tubercularis</i>	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Crisilla postrema</i>	0	31	0	9	0	0	87	0	0	16	0	17	0	0	0	8	0	55	0	0	0
<i>Eulima</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55	0	0	0
<i>Crassadoma pusio</i> = <i>H. distortus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	263	55	0	0
<i>Jujubinus exasperatus</i>	0	0	0	18	0	34	0	0	0	16	0	0	0	0	0	0	0	0	276	0	15
<i>Jujubinus pseudogravinae</i>	0	16	17	0	22	0	43	0	24	0	0	0	0	0	0	0	0	0	0	0	0
<i>Jujubinus striatus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	55	0	0
<i>Jujubinus</i> sp.	15	0	0	23	0	17	0	0	0	0	0	0	0	0	0	0	0	0	526	55	0
<i>Manzonia unifasciata</i>	29	0	0	5	0	0	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Mitrolunna</i> sp.	0	0	0	0	0	0	0	0	0	24	16	0	17	0	0	0	0	0	0	0	0
<i>Ocinebrina aciculata</i>	0	0	0	9	22	17	0	40	24	64	0	35	0	0	0	0	0	166	0	0	0
<i>Odostomia</i> sp.	0	0	0	0	0	0	22	40	0	0	27	0	0	0	0	0	0	0	0	0	0
<i>Odostomella dolilolum</i>	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0
<i>Omalogyra atomus</i>	0	0	0	0	0	0	0	0	0	0	64	27	0	0	0	0	0	0	0	0	0
<i>Paricardium vroomi</i>	88	0	0	5	261	0	0	0	0	0	27	0	0	0	0	0	0	0	0	0	0
<i>Plagiocardium papillosum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Pollia dorbignyi</i>	0	0	0	0	0	0	43	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Raphitoma</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Raphitoma linearis</i>	0	0	0	9	0	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Rissoa guernei</i>	59	16	17	283	566	85	0	0	0	16	0	0	0	130	166	0	0	0	0	294	120
<i>Setia</i> sp.	59	0	14	0	0	217	121	190	32	54	17	0	0	0	0	0	0	0	0	0	11
<i>Setia subvaricosa</i>	29	172	0	59	0	34	2,928	2,429	1,734	1,202	432	708	5	31	158	263	0	0	204	97	215
<i>Sinezona cingulata</i>	0	0	17	0	0	0	22	0	0	16	0	17	0	0	0	0	0	0	0	0	0
<i>Trichomusculus semigranatus</i>	0	455	294	178	349	34	456	324	285	288	270	276	0	0	8	526	110	244	60	46	57
<i>Triphora</i> sp.	0	16	0	0	22	17	22	0	0	32	0	17	0	0	0	0	55	0	0	0	0
TOTAL	16,191	1,583	882	12,449	17,298	6,142	7,354	5,020	11,805	6,394	10,973	7,547	56	265	482	3,947	18,177	15,122	2,142	1,304	6,206