Proc. NIPR Symp. Polar Biol., 9, 283–298, 1996

ANALYSIS OF SOIL MICROBIAL COMMUNITIES (AUTOTROPHS AND HETEROTROPHS) FROM KING GEORGE ISLAND (ARCTOWSKI STATION)

Manfred BÖLTER

Institut für Polarökologie, Universität Kiel, Wischhofstr. 1–3, Ged. 12, D-24148 Kiel, F.R. Germany

Abstract: Microbial communities of Antarctic soils are analysed with regard to their structures and compositions of microautotrophs and microheterotrophs. Size classes of bacteria and morphotypes of autotrophs are used as descriptors of samples from soils and plants. This matrix (31 samples × 37 descriptors) is clustered in R- and Q-modes. The clusters of samples are defined by their descriptors which have specific significance: Several parameters, *e.g.* bacterial mean cell volume, fractions of rod shaped bacteria, can be used as discriminators for individual sites and their specific microbial communities. The results are discussed in relation to community studies of other sites.

1. Introduction

The terrestrial environment in the vicinity of Arctowski Station on King George Island shows very different habitats. Climatic and edaphic effects lead to mosaics of vegetation types including fellfield systems with barren soils, lichen heaths on the moraine lines, wet areas with large stands of mosses, and meadows with *Deschampsia antarctica* and *Colobanthus quitensis* (OLECH, 1993; ZARZYCKI, 1993; FABISZEWSKI and WOJTUN, 1993).

Microbial communities are important links between organic and inorganic matter on the one hand and living biomass on the other hand, especially in these environments where meiofaunal components are scarce. Microarthropods, mites, nematodes and other lower organisms have only limited abundances, they occur only in sheltered environments, and pose only small predatory pressure (BLOCK, 1984).

Such habitats with short food chains and direct links between autotrophs and microheterotrophs are of interest for studies between these components and their relationships to environmental variables. This presents a promising area for research in soils and its developments at different stages.

The purpose of my studies during the last few years has been comparisons between soils and plants from the view of microbial colonization and therewith related microbial activity (BÖLTER, 1989, 1990a, 1992a, b, 1993). Since descriptive papers of these environments and its microbial communities have been published recently (BÖLTER, 1995a, b), this study focuses on the relationships between individual parameters of the bacterial community and descriptors of sites by multivariate analyses.

2. Materials and Methods

2.1. Sampling

Samples were taken from various sites on King George Island in the vicinity of Arctowski Station. The sites are located in different environments of the Admiralty Bay area (Fig. 1, Table 1).

Colonization of microorganisms on plants and soil surfaces was analysed on samples from sites 1–10 (depth of 0 to 2.5 cm), and a patch (≈ 2 m^2) of diverse plant

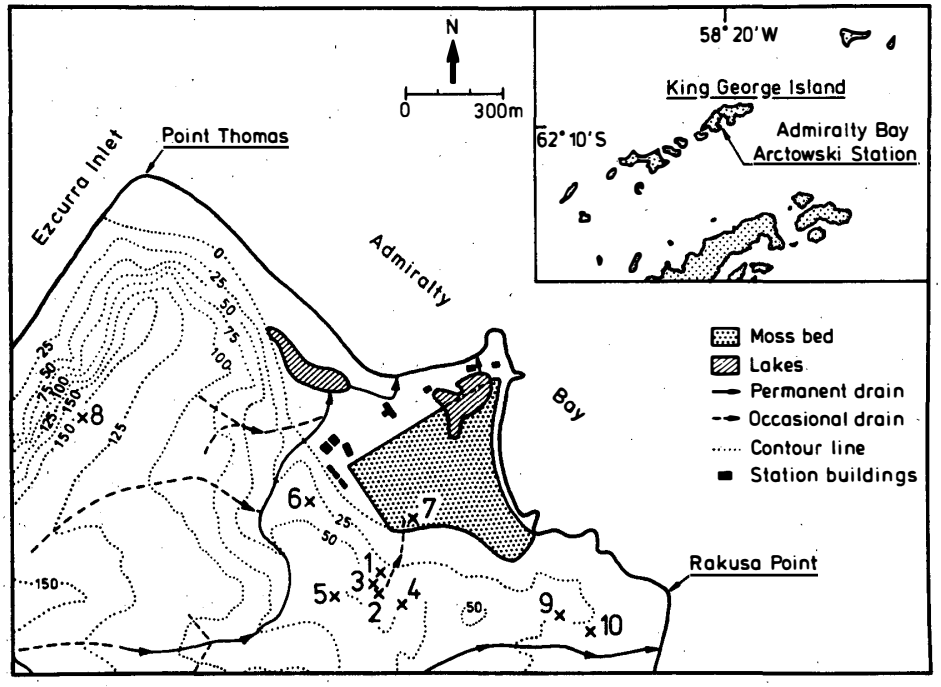

Fig. 1. Map of the sampling locations at King George Island, Antarctica (after RAKUSA-SUSZCZEWSKI *and* KRZYSZOWSKA, *1991).*

Table 1. Site descriptions for samplings can be given as follows.

Site 1:	Meadow with dense plant cover of *Deschampsia antarctica* and *Colobanthus quitensis*, as well as some moss cushions (*Drepanocladus uncinatus*, *Polytrichum* sp.);
Site 2:	Mineral soil lacking plant cover;
Site 3:	Moss cushions of *Drepanocladus uncinatus*, covered with the epiphyic lichen *Ochrolechia frigida;*
Site 4:	A meadow of *Deschampsia antarctica* and *Colobanthus quitensis*, with few cushions of *Drepanocladus uncinatus;*
Site 5:	Barren soil in-between some rocks and stones covered with *Usnea antarctica*, alt. *ca.* 50 m a.s.l.; close to this are some spots with *D. antarctica*, *C. quitensis* and few cushions of *D. uncinatus;*
Site 6:	Barren muddy soil, no plant cover, altitude *ca.* 40 m a.s.l.;
Site 7:	Wet waterlogged plain with mainly *D. uncinatus* and *Polytrichum* sp., at sea level;
Site 8:	Barren soil from a large plain at Panorama Ridge, altitude *ca.* 150 m a.s.l.;
Site 9:	Moraine near Ecology Glacier with a well-established cover of lichens (mainly *Usnea antarctica*, *O. frigida*, *Buellia caniops*, *B.* sp., *Rhizocarpon geographicum*, *Lepraria neglecta)* and mosses (mainly *D. uncinatus*), some higher plants (*D. antarctica* and *C. quitensis*), altitude about 30 m a.s.l.;
Site 10:	Moraine close to Ecology Glacier, no plant cover, altitude about 20 m a.s.l.

Table 2. Sample descriptions for the analysis of soil phototrophs, sites as given in Fig. 1.

Sample No.	Site	Sample description and depth or plant species
51	2	soil, 0–0.5 cm[1]
52	2	soil, 0.5–1.5 cm[1]
53	2	soil, 1.5–2.5 cm[1]
54	2	soil, 2.5–3.5 cm[1]
64	1	plant horizon, +0–+1.5 cm[1]
65	1	soil, 0–0.5 cm[1]
66	1	soil, 0.5–1.5 cm[1]
67	1	soil, 1.5–2.5 cm[1]
78	1	shoot of *Deschampsia antarctica*
79	1	root (0.5–2.5 cm) of *D. antarctica*
80	5	shoot of *D. antarctica*
81	5	root (0.5–2.5 cm) of *D. antarctica*
83	1	shoot of *Colobanthus quitensis*
84	1	root of *C. quitensis*
85	5	shoot of *C. quitensis*
86	5	root of *C. quitensis*
87	5	dry moss covered with *Ochrolechia frigida*
88	5	fresh moss (*Polytrichum* sp.)
90	4	dry moss covered with *Ochrolechia* sp.
91	7	moss bed (*Drepanocladus uncinatus)*
92	5	*Usnea antarctica*
93	5	*U. antarctica*
96	9	*O. frigida*
97	5	*Placopsis contortuplicata*
98	2	soil, 0–0.5 cm
99	3	soil, 0–0.5 cm
100	5	soil, 0–0.5 cm
101	6	soil, 0–0.5 cm
102	8	soil, 0–0.5 cm
103	10	soil, 0–0.5 cm
104	5	soil, 0–0.5 cm

[1]samples 51–54 are from profile DP1 and samples 64–67 are from profiles DP2 (see text).

cover (close to site 5) including *Deschampsia antarctica, Colobanthus quitensis, Usnea antarctica, Polytrichum* sp., *Drepanocladus uncinatus* with *Ochrolechia frigida* and *Candelariella vitellina,* and *Placopsis contortuplicata;* altitude is about 30 m a.s.l. Two sites, close to sites 1 and 2 (named DP1 and DP2), were sampled in 1 cm steps from surface layers down to 12.5 cm. A description of all sampling sites is given in Table 2.

The data used for this study are part of a more comprehensive data set which includes in total 104 samples from the sites described in Table 1 (BÖLTER, 1995a, b), it refers only to those samples where algae were monitored, *i.e.* 31 samples.

2.2. Analyses

All analyses except those for organic matter and plant pigments were performed in the station's laboratory. Methods of analyses of climatic conditions, soil properties (pH, contents of water, stones, organic matter) C/N-ratio, plant pigments and of the bacterial communities followed standard procedures and have been published recently by BÖLTER (1995a, b). In total, 37 descriptive parameters are included in this study (Table 3).

Table 3. Descriptors (abbrevations and dimensions) used for the cluster analysis.

[1] water content (%H_2O of f.wt)
[2] total bacterial counts (TBN, 10^8 g^{-1} d.wt)
[3] total bacterial biomass (TBB, μg C g^{-1} d.wt)
[4] bacterial mean cell volume (MCV, μm^3)
[5] counts of cocci <0.5 μm (% of TBN)
[6] counts of cocci 0.5–1 μm (% of TBN)
[7] counts of cocci >1.0 μm (% of TBN)
[8] counts of cocci >0.5 μm (% of TBN)
[9] counts of rods 0.5–1 μm (% of TBN)
[10] counts of rods 1.0–2.0 μm (% of TBN)
[11] counts of rods 2.0–3.0 μm (% of TBN)
[12] counts of rods >3.0 μm (% of TBN)
[13] counts of rods 0.5–2.0 μm (% of TBN)
[14] counts of rods >2.0 μm (% of TBN)
[15–24] amounts of bacterial size classes (% of TBB) as above [5–14]
[25] total counts of phototrophs (TAN, 10^6 g^{-1} d.wt)
[26] total phototroph biovolume (TAB, 10^9 μm^3 g^{-1} d.wt)
[27] phototroph biovolume *vs.* bacterial biovolume (TAV/BBV)
[28] sum of phototroph biovolume + bacterial biovolume (TBV, 10^9 μm^3 g^{-1} d.wt)
[29] % bacterial biovolume of TBV
morphotypes of phototrophs
[30] cylinders (% of TAN)
[31] cylinders (% of TAB)
[32] ellipsoids (% of TAN)
[33] ellipsoids (% of TAB)
[34] coccoids (% of TAN)
[35] coccoids (% of TAB)
[36] filaments (% of TAN)
[37] filaments (% of TAB)

2.3. Data analysis

The data set comprises 31 samples (Table 2) and 37 parameters (Table 3). Cluster analysis was carried out by a program "COMM" (PIEPENBURG and PIATKOWSKI, 1992). Cluster algorithms used for this study were: single linkage, complete linkage, unweighted and weighted pair group method using arithmetic averages. The Spearman rank correlation coefficient served as a similarity index. The matrix was analysed in R- and Q-modes in order to evaluate groups of parameters or samples. The sign of the correlation coefficient was neglected for the description of the groups; thus it was only looked at for the existence of correlations between individual parameters.

As no "objective" criteria can be defined for the acceptance of individual clusters, only empirical definitions of groups of parameters or sites can be used for their establishment. Hence, some arbitrariness has to be taken into consideration when thresholds are set for dividing objects into clusters, although statistical procedures can be used to verify those groups (BÖLTER, 1990b).

3. Results

3.1. Environmental properties

Environmental properties and soil characteristics are given in detail by BÖLTER

(1995a, b). In general, pH-values increase with depth, maximal content of organic matter is found in surface layers with active plant cover, high C/N ratios (>20) are mainly concomitant to high amounts of organic matter, and low C/N ratios (<10) are found in connection with low amounts of organic matter.

3.2. Bacteria

Bacterial counts (TBN) and biomass (TBB) are presented in detail in the papers of BÖLTER (1995a, b). Data of TBN and TBB are highest in soil surface samples with high amounts of organic matter and on surfaces of vascular plants (samples 64–67), samples of plants (*Deschampsia antarctica, Colobanthus quitensis,* shoots and roots, samples 78–86) and on mosses (samples 87–91). Lichens (samples 92–97) show very low values, comparable to those of barren soils. Surface samples (0–0.5 cm) 99, 100 and 104 show maxima of the uppermost soil surface samples (98–104).

The concomitant pattern of the MCV is more heterogeneous and does not reflect such a significant trend. As such, MCV on surfaces of *D. antarctica* and *C. quitensis* and mosses (samples 78–91) are generally higher than those of related roots. High values of MCV are also found in soil samples 102 and 104 and on the samples of *Usnea antarctica* (93) and *Placopsis contortuplicata* (97).

Small cocci ($<0.5\ \mu m$) are found only in low amounts in soil samples (51–67, 98–104), samples of roots from *D. antarctica, C. quitensis,* samples of mosses, microlichens and on samples of *Usneas.* Large rods ($>2\ \mu m$) are found mainly on surfaces of plants or roots. This fraction, however, is of minor importance for soils (except sample 102).

Plant samples have higher amounts of rods 1–2 μm than soils (except samples 102, 103, 104). Further details are given in BÖLTER (1995a).

3.3. Phototrophs

Phototrophs (cyanobacteria and eucaryotic algae) were monitored only on surfaces of plant samples and in soil surfaces to a maximal depth of 2.5 cm (*e.g.* sample 67). Typically, a steady decrease of these organisms can be shown by samples of profiles DP1 (51–54) and DP2 (64–67).

Highest counts and biovolumes of phototrophs are found on plant surfaces (*D. antarctica, C. quitensis,* and mosses). Shoots of *D. antarctica* and *C. quitensis* show counts of phototrophs in the range between 10×10^3 and 54×10^3 cells g^{-1}; root systems show a range between 0.5×10^3 and 11.2×10^3 cells g^{-1}. Mosses show algal counts between 4.6×10^3 and 76×10^3 cells g^{-1}. Soil surfaces show fairly constant values between 14×10^3 and 44×10^3 cells g^{-1}. Fruticose lichens (*U. antarctica, U. aurantiaco-atra*) were only poorly or even not colonized by phototrophs.

Great variability in the distributions of the morphotypes of algae and cyanobacteria is found for the individual samples compared to the microscopic counts. Soil samples are governed mainly by small coccoid phototrophs (up to 90% of the total community, sample 102). These forms, however, did not show a significant contribution to the total biovolume of phototrophs. Cylindric and ellipsoid forms represent the dominant community on plant surfaces. Filamentous forms with high contributions ($>50\%$) to total biovolume are found only in soil samples of sites 3 and 10, as well as in the root system of *C. quitensis,* and on the lichens *P. contortuplicata* and *U. antarctica.*

Relationships between phototroph biovolume and bacterial biovolume show a dominance of bacteria (>50%) of the total biovolume (TBV) in most soil samples (except surface layer of sites 2 and DP1, and most root systems). Ratios near between 0.25 and 1 are found in surface samples of sites 1, 2, 4, 5, 6, 8, 10, and on shoots of *C. quitensis.*

Comparisons of biovolumes from phototrophs and heterotrophs (bacteria) show that the biovolume of heterotrophs represents 15.7% of the total biovolume (phototrophs + heterotrophs) in sample 51, and 54.4% in sample 65. At deeper levels (where algae are present) those figures rise to 80 and 85%, respectively. Shoots of *D. antarctica* have 3–12% bacterial biovolume, shoots of *C. quitensis* 48–52% bacterial biovolume of total biovolume (phototrophs + heterotrophs). Corresponding root systems have 10–99% bacterial biovolume, depending on depth. Mosses (*Drepanocladus uncinatus, Polytrichum* sp.) showed bacterial abundance between 26 and 96%, whereas lichens had mainly more than 90% bacteria of total epiphytic cover.

The morphotypes show that soil surfaces (0–0.5 cm) are dominated by coccoid and filamentous cells. Deeper layers contained cylindric and ellipsoid forms in greater amounts.

In terms of biovolume, coccoid forms are of minor importance. This holds especially true for plant surfaces (shoots and roots) where the algal biovolume is represented mainly by ellipsoids and cylindrical forms. Exceptions can be found only with one root of *C. quitensis* (100% filaments) and a moss cushion which is overgrown with *Ochrolechia frigida,* where cylindrical, coccoid and filamentous forms shared the algal biovolume to equivalent parts. No cylindrical or ellipsoid forms are found on fruticose lichens (*U. antarctica*) which indicates that these plants differ significantly from other plants with respect to their epiphytic community.

3.4. Cluster analysis

a) Parameters

According to the four cluster algorithms, the different results of these procedures and a summary of them are presented in Table 4. Five large groups (G1, G2, G3, G5, G6) can be accepted as consistent during all cluster procedures besides several pairs (G4, G7, G8, G9) of parameters because their members can be found closely related to each other during all linkages of the different cluster procedures.

The main results from this analysis are:

- Mean cell volume of bacteria (MCV) is closely related to counts and biovolumes of rod shaped bacteria. They are not influenced by any abundance of coccoid bacteria or of phototrophs (Group 1).
- Total count and biomass of bacteria as well as total biovolume of bacteria and algae are closely interrelated and related to actual water content (Group 2).
- Counts and biovolume of phototrophs are influenced by filamentous phototrophs; they also influence the portion of bacteria of the total microbial biovolume (Group 3).
- Elliptic shaped cells are not influenced/ do not influence other parameters (Group 4).
- Coccoid bacteria larger than 0.5 μm (counts and biovolume) are independent groups (Group 5).
- Large coccoid forms (bacteria and algae) are related to each other. This points to a

Table 4. Groups (G) of parameters (PAR, for identification of numbers see Table 3) established by the cluster algorithms single linkage (SL), complete linkage (CL), unweighted pair group method using arithmetic averages (UPGMA) and weighted pair group method using arithmetic averages (WPGMA). Groups are numbered and subgroups are specified by letters. Threshold for cluster definition was 0.492 ($n=37$, $p<0.01$). For criteria for acceptance of groups see text.

SL		CL		UPGMA		WPGMA		Accepted as stabile group	
PAR	G	PAR	G	PAR	G	PAR	G	PAR	G
11	1a	11	1a	11	1a	11	1a	11	1
14		14		14		14		14	
21		21		21		21		21	
24		24		24		24		24	
		23						9	
4	1b			9	1b	9	1b	19	
10		9	1b	19		19		4	
23		19						10	
				4	1c	4	1c	23	
9	1c	4	1c	10		10			
19		10		23		23			
								2	2
2	1d	2	2	2	2	2	2	3	
3		3		3		3		28	
28		1		28		28		1	
26					1		1		
29		26	3						
25		28		26	3	26	3	26	3
1		25		29		29		29	
37				37		37		37	
36		6	4	25		25		25	
		8		36		36		36	
6	1e	16							
8		18		32	4	32	4	32	4
16				33		33		33	
18		32	5						
		33		13	5	6	5	6	5
13	2			20		8		8	
20		7	6			16		16	
		17		5	6	18		18	
5	3			15					
15		12	7			7	6	7	6
		22		6	7	17		17	
7	4			8		35		35	
17		13	8	16		34		34	
		20		18					
								12	7
12	5					12	7	22	
22		5	9	7	8	22			
		15		17				13	8
				35		13	8	20	
		29	10			20			
		37		12	9			5	9
				22		5	9	15	
						15			

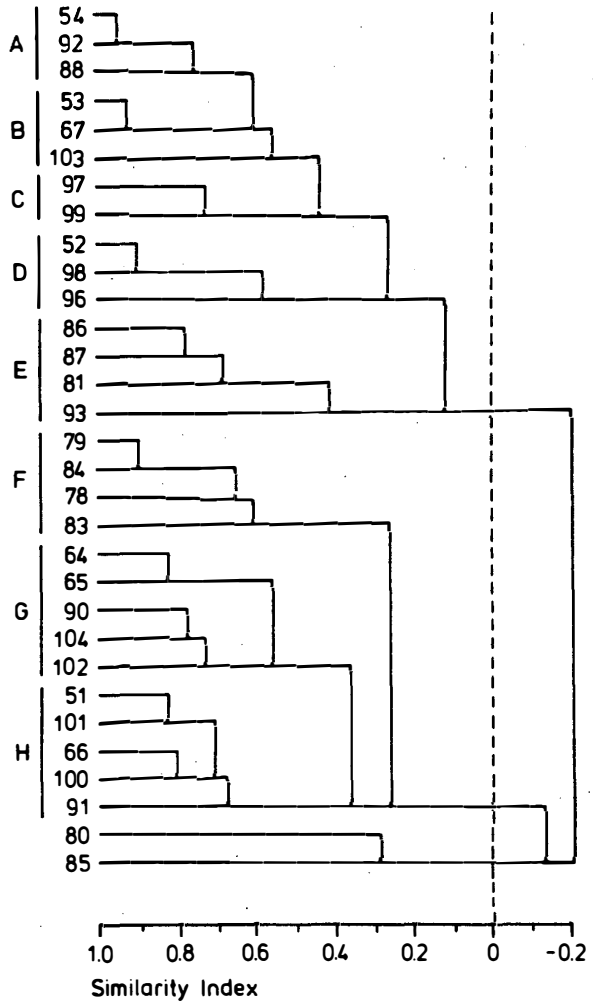

Fig. 2. Dendrogram of samples (complete linkgae clustering). The similarity index is the Spearman-rank correlation coefficient.

methodological problem, *i.e.* the discrimination between autotrophs and heterotrophs in this size class (Group 6).

- Counts and biomass of large rod shaped bacteria, small cocci and two classes of small rod shaped bacteria remain unlinked to other parameters (Groups 7–9).
- Three further descriptive parameters of the bacterial community remain ungrouped.

b) Samples

Figure 2 presents the dendrogram of the complete linkage clustering and shows the main discriminations between groups of samples. Most of the established groups appear in the same form in the other cluster algorithms. Some are enlarged by individual samples, mainly the single linkage clustering melts several groups at lower levels.

It is evident from this analysis that samples from various origins may clump together as one cluster. For example, Group A combines a sample from the soil profile, from a moss sample and a lichen sample. Although the other groups are more homogeneous, mixtures of soil and plant samples are common and the separation between the large groups I and II cannot be verified from the locations of the samples alone, *e.g.* Groups E and G.

Table 5. Parameters (minima, mean values [m], maxima), of the total data file and those describing groups A–H, where $3 \times s < m$ and which thus can be used as descriptors of groups as established from cluster analysis (see Fig. 2; for dimensions of parameters refer to Table 3).

Parameter	All data	Groups A	B	C	D	E	F	G	H
[1] %H_2O	1.00[1]					12.60			
	22.00[2]					14.15			
	75.00[3]					15.80			
[2] TBN	0.10				0.94	4.94			
	6.11				1.14	7.14			
	24.49				1.34	8.65			
[3] TBB	0.23				1.33				
	20.97				1.56				
	89.27				1.77				
[4] MCV	0.11		0.11	0.20	0.12	0.26	0.17	0.29	
	0.30		0.12	0.25	0.14	0.35	0.21	0.45	
	0.61		0.14	0.30	0.16	0.49	0.27	0.60	
[5] Cocci $<0.5\ \mu$m (%n)	0.0		28.75	18.25	20.50	8.75	16.50		
	16.92		32.92	18.88	24.83	11.58	23.26		
	40.00		38.00	19.50	29.50	13.75	19.55		
[6] Cocci 0.5–1 μm (%n)	0.0	1.50			2.75				
	3.31	1.92			4.85				
	13.00	2.25			6.50				
[7] Cocci $>1\ \mu$m (%n)	0.0	0.0	0.0			0.0	0.0	0.0	
	0.26								
	2.25								
[8] Cocci $>0.5\ \mu$m (%n)	0.0	1.50							
	3.60	1.92							
	15.25	2.25							
[9] Rods 0.5–1 μm (%n)	0.0	25.25	48.25	29.75	54.50	17.00	38.00		
	36.55	39.75	51.18	38.38	56.77	31.00	45.65		
	58.80	49.25	54.30	47.00	58.80	39.00	57.50		
[10] Rods 1–2 μm (%n)	6.75			24.00	9.25	36.00	13.30		12.50
	30.40			25.25	11.42	40.00	19.37		28.62
	67.80			26.50	14.00	45.25	31.30		39.80
[11] Rods 2–3 μm (%n)	0.0				1.50				
	10.67				1.83				
	30.50				2.50				
[12] Rods $>3\ \mu$m (%n)	0.0		0.0		0.0				
	1.94								
	7.75								
[13] Rods 0.5–2 μm (%n)	48.30	56.00	58.00	56.25	65.50	62.25	57.75	62.30	48.30
	66.95	69.08	64.52	63.63	68.18	71.00	65.02	67.65	64.02
	79.00	79.00	67.80	71.00	72.80	75.75	70.80	72.50	73.75

[1]min, [2]mean, [3]max

Table 5 (Continued).

Parameter	All data	Groups A	B	C	D	E	F	G	H
[14] Rods >2 μm (%n)	0.0				1.50				
	12.61				1.83				
	36.50				2.50				
[15] Cocci <0.5 μm (%v)	0.0		0.85	0.25	0.60		0.30		
	0.42		1.18	0.33	0.78		0.48		
	1.53		1.50	0.40	1.05		0.55		
[16] Cocci 0.5–1 μm (%v)	0.0			0.30	4.19				
	2.71			4.30	6.16				
	7.75			7.75	7.60				
[17] Cocci >1 μm (%v)	0.0	0.0	0.0			0.0	0.0	0.0	
	1.72								
	13.17								
[18] Cocci >0.5 μm	0.0								
	4.43								
	20.92								
[19] Rods 0.5–1 μm	0.0		38.45		40.20		15.90		
	22.23		49.25		47.49		25.83		
	54.90		54.61		54.98		39.70		
[20] Rods 1–2 μm	22.52		24.14	32.21	26.10	33.61	27.20	33.80	23.40
	36.82		39.36	38.46	30.37	45.07	32.77	36.60	32.41
	54.65		50.14	44.70	36.30	50.98	42.10	42.90	43.70
[21] Rods 2–3 μm	0.0	17.84		18.80	9.20	21.02	18.50	30.30	
	26.03	22.34		22.04	11.46	29.15	27.26	38.20	
	48.40	30.23		25.28	14.10	39.27	36.67	44.10	
[22] Rods >3 μm	0.0		0.0		0.0			13.60	
	10.08							16.05	
	25.76							20.20	
[23] Rods 0.5–2 μm	26.70	45.76	78.75	43.44	66.30	37.53	77.88	35.30	26.70
	59.05	65.38	88.61	57.67	77.87	57.10	58.10	44.35	48.13
	98.40	76.83	98.40	71.90	83.70	68.13	69.13	51.20	63.37
[24] Rods >2 μm	0.0			18.80	9.20		24.70	46.20	27.68
	36.11			27.10	11.46		37.50	54.25	43.94
	70.00			35.39	14.10		50.17	64.30	70.80
[25] Algae (TAN)	0.25								
	65.25								
	1314								
[26] Algae (TAB)	0.26			2.65					
	639.8			3.76					
	6639			4.88					
[27] TAV/BBV	0.0			0.07					0.43
	2.95			0.09					0.67
	30.08			0.11					0.95

Table 5 (Continued).

Parameter	All data	Groups A	B	C	D	E	F	G	H
[28] TAV+BBV	2.52								
	849.0								
	7329								
[29] %BBV of [28]	2.63	80.23	65.29	90.03		95.72			51.17
	61.18	87.44	75.30	91.79		97.79			60.87
	99.79	92.53	85.55	93.56		99.79			70.13
[30] Cyl. %TAN	0.0			0.0					
	24.27								
	100.0								
[31] Cyl. %TAB	0.0			0.0					
	21.13								
	100.0								
[32] Ell. %TAN	0.0	0.0		0.0					
	17.95								
	100.0								
[33] Ell. %TAB	0.0	0.0		0.0				79.09	36.11
	52.83							91.10	70.26
	100.0							97.37	89.85
[34] Coc. %TAN	0.0	0.0		55.47			45.68	0.0	
	32.61			60.43			64.97		
	400.0			65.38			78.57		
[35] Coc. %TAB	0.0	0.0		9.00				0.0	
	3.89			9.26					
	100.0			9.51					
[36] Fil. %TAN	0.0			34.61					
	25.17			39.58					
	100.0			44.54					
[37] Fil. %TAB	0.0			90.48					
	25.15			90.74					
	100.0			91.00					

Thus, the question arises about the significance of this separation. This can be answered by the study of those parameters which may be used to describe the established groups. Table 5 shows those parameters which can be used as valid descriptors. They are reduced within their spans and their standard deviation (s) in relation to the original data set either by the mean value (m) [$3 \times s < m$] or by those individual parameters, such as some groups of bacteria or algae, which are not found on some of these groups.

Such discriminations by parameters become evident *e.g.* from MCV, various groups of rods or others. Some groups of samples are described by only few descriptors which depreciated the spans of individual parameters which than become descriptive, *e.g.* water content in Group E.

4. Discussion

The data presented give a detailed picture of the microbial environment in Antarctic soils, bacteria and phototrophic organisms, which are important factors for the description and understanding of processes in this environment.

4.1. Microbiological characteristics

The bacterial counts found in these samples (10^8 to 10^9 per gram soil) are somewhat lower than reported from other studies in Antarctic soils (*e.g.* RAMSAY, 1983; WYNN-WILLIAMS, 1985; RAMSAY and STANNARD, 1986; HEATWOLE *et al.*, 1989; ROSER *et al.*, 1993), but they match well with data from earlier studies in this Antarctic habitat (BÖLTER, 1990a, 1992a, b).

Since methodological constraints have to be taken into account for direct comparisons of such data, ratios between individual parameters are more meaningful. The high values for MCV, which are generally related to soil depth levels with high contents of organic matter and/or plant cover, show that significant divisions can be related to edaphically rich and poor sites. This is comparable to results from FRENCH and SMITH (1986) from Marion Island.

Counts of phototrophs vary between 10^2 and 10^5 per gram dry weight. They are found in soil surfaces and on plants as epiphytes. These results correspond to analyses of other authors who have also found the highest numbers on plants (*e.g.* BROADY, 1979a, b, 1982, 1989; OHTANI and KANDA, 1987; OHTANI *et al.*, 1991) or in relation to soil particles (*e.g.* DAVEY *et al.*, 1991) where algae and cyanobacteria play an important role in the stabilization of fellfield soils. Further, high counts of phototrophs are found below herbacerous vegetation and highest at places with *D. antarctica* and *C. quitensis* rather than at places with mosses (*e.g. D. uncinatus;* BROADY, 1979a).

The data shown of bacteria in relation to total microbial biovolume (parameter 29, Table 5) can be compared with those from ROSER *et al.* (1992), who finds 92% of microbial biomass of soils of a penguin colony due to bacteria and 4–22% bacteria in other soils.

Analyses of algal communities in comparable soils have shown that diatoms and cyanobacteria are dominating groups (BROADY, 1979a, b; DAVEY, 1988). However, direct comparisons between those data are difficult, because many data were obtained mainly by culture counts of algal propagules or other semiquantative techniques– although similar trends were shown at Signy Island (BROADY, 1979a).

4.2. Multivariate analysis

The results of the cluster analysis of parameters which describe the samples by different properties showed clearly that differences have to be drawn between those of the bacterial (heterotrophic) community and the phototrophs. No direct links were found between these groups from the cluster analyses. This means that the communities act indepently from each other.

The main descriptor of the bacterial community evidently is the mean cell volume which is influenced primarily by some groups of rods but not related to total count or total biomass. These latter descriptors are more closely related to the actual water

content and the total microbial biovolume. Although this points to direct relationships between moisture and microbial organisms, this relationship cannot be seen with individual floral compounds. This fact can only be understood considering that there are no direct links between these components and that we need more detailed informations about microbially mediated processes in soil ecosystems–which are still poorly understood (O'DONNELL *et al.*, 1994). This holds true for the roles of coccoid shaped bacteria but also for individual groups of phototrophs.

The analysis of the samples and further view on the description of the sample's groups (Table 5) shows that preliminary discriminations into different soil samples or plant samples may be very arbitrarily– at least when considering the total data file. This splitting into different acting units shows on the other hand the flexibility of total community, which can be explained by different nutrient stages supporting individual bacterial or algal groups. As quantifications by cultural methods are diffcult and yield only small and skewed selections of organims, concepts of species shifts and succesions are limited (O'DONNELL *et al.*, 1994) and system descriptions of ecosystems at this level remain difficult.

4.3. Conclusion

The approach followed during this study was descriptive. Although some interactions become clarified by the results, most reasons for variability in these systems remain hidden because of the non understood matrix of complexity of the soil environment, its fluctuations and dynamics. Strong variability, at even small scales (<0.013 m) was described for spatial heterogeneity of algae in soil crusts in Colorado (GRONDIN and JOHANSEN, 1993) as in polygon (625 cm^2) at Signy Island (WYNN-WILLIAMS, 1993).

Methodological restrictions serve for further limitations as individual parameters highlight only very thin levels of the organisms in the microbial food web. Complete analysis of this still remains a challenge in microbial ecology considering methods of isolation or microscopical inspection. This fact also restricts application of biodiversity models valid for the higher organisms to the microbial community (O'DONNELL *et al.*, 1994).

There still now remains the question about the postulated relationships between autotrophic and heterotrophic organisms. The results of this study may suggest a clear "no" because of the absence of interactions between bacteria and algae in the cluster analysis. This, however, tells only half of the truth because more data are needed either to neglect such relationships or to verify them by adequate methods and data sets. One main fact during this study can be seen in the different scales of the levels of heterotrophs and autotrophs–it can be argued that such mismatches are responsiple for obvious but missing relationships. There is no doubt that primary succession in these environments is goverened by microbes (WYNN-WILLIAMS, 1993) and that soil microstructure is effected directy by algae and/or cyanobacteria (BELNAP and GARDNER, 1993).

The analysis of microbial systems needs the application of appropriate in temporal and spatial scales, a fact which leads to further complication in resolutions and the extrapolation of results from microscopical studies in order to elucidate information about the effects of environmental properties and the relationship between population diversity and function (KLUG and TIEDJE, 1994).

The application of microscopic techniques and therewith connected image analysis will provide possibilities to analyse more samples and give at least more statistical reliability at the scales which have to be investigated. Such approaches should be made available to studies in soil ecology more routinely. Methodological rules and results of natural bacterial (BÖLTER *et al.*, 1993) or bacterial/cyanobacterial assemblages (WYNN-WILLIAMS, 1988, 1990, 1992) from Antarctic soils provide steps into this direction and should be used more routinely in such micro-ecological studies.

Acknowledgments

I am greatly indepted to the Polish Academy of Science who provided me the visit to the Antarctic Station H. Arctowski on King George Island during December/ January 1992/93 (16th and 17th expedition) and especially to Dr. A.M. OLECH for kind cooperation during my field work and the determinations of plant species. I also thank the crew of the M/S COLUMBUS CARAVELLE for their kind logistic support. My thanks go further to Drs. P. BROADY, R. GRADINGER and S. OHTANI who gave valuable comments on this data set. The study was financially supported by the Deutsche Forschungsgemeinschaft (Bo 918/4).

References

BELNAP, J. and GARDNER, J.S. (1993): Soil microstructure in soils of the Colorado Plateau: The role of the cyanobacterium *Microcoleus vaginatus*. Great Basin Nat., **53**, 40–47.

BLOCK, W. (1984): Terrestrial microbiology, invertebrates and ecosystems. Antarctic Ecology, ed. by R.M. LAWS. London, Academic Press, 163–236.

BÖLTER, M. (1989): Microbial activity in soils from Antarctica (Casey Station, Wilkes Land). Proc. NIPR Symp. Polar Biol., **2**, 146–153.

BÖLTER, M. (1990a): Microbial ecology of soils from Wilkes Land, Antarctica: I. The bacterial poulation and its activity in relation to dissolved organic matter. Proc. NIPR Symp. Polar Biol., **3**, 104–119.

BÖLTER, M. (1990b): Evaluation –by cluster analysis– of descriptors for the establishment of significant subunits in Antarctic soils. Ecol. Modelling, **50**, 79–94.

BÖLTER, M. (1992a): Vergleichende Untersuchungen zur mikrobiellen Aktivität in Böden und an Kryprogamen aus der kontinentalen und maritimen Antarktis. Habilitationsschrift, University Kiel, 202 p. (unpublished).

BÖLTER, M. (1992b): Environmental conditions and microbiological properties from soils and lichens from Antarctica (Casey Station, Wilkes Land). Polar Biol., **11**, 591–599.

BÖLTER, M. (1993): Effects of carbohydrates and leucine on growth of bacteria from Antarctic soils (Casey Station, Wilkes Land). Polar Biol., **13**, 297–306.

BÖLTER, M. (1995a): Distributions of bacterial numbers and biomass in soils and on plants from King George Island (Arctowski Station, Maritime Antarctic). Polar Biol., **15**, 115–124.

BÖLTER, M. (1995b): Microbial communities in soils and on plants from King George Island (Arctowski Station, Maritime Antarctica). Proc. VI SCAR Symposium Venice 1994 (in press)

BÖLTER, M., MÖLLER, R. and DZOMLA, W. (1993): Determination of bacterial biovolume with epifluorescence microscopy: Comparison of size distributions from image analysis and size classifications. Micron, **24**, 31–40.

BROADY, P.A. (1979a): Quantitative studies on the terrestrial algae of Signy Island, South Orkney Islands. Br. Antarct. Surv. Bull., **47**, 31–41.

BROADY, P.A. (1979b): A preliminary survey of the terrestrial algae of the Antarctic Peninsula and South Georgia. Br. Antarct. Surv. Bull., **48**, 47–70.

BROADY, P.A. (1982): Ecology of non-marine algae at Mawson Rock, Antarctica. Nova Hedwigia, **36,** 209–229.

BROADY, P.A. (1989): Survey of algae and other terrestrial biota at Edward VII Peninsula, Marie Byrd Land. Antarct. Sci., **1,** 215–224.

DAVEY, M.C. (1988): Ecology of terrestrial algae of the fellfield ecosystems of Signy Island, South Orkney Islands. Br. Antarct. Surv. Bull., **81,** 69–74.

DAVEY, M.C., DAVIDSON, H.P.B., RICHARD, K.J. and WYNN-WILLIAMS, D.D. (1991): Attachment and growth of Anatrctic soil cyanobacteria and algae on natural and artificial substrata. Soil Biol. Biochem., **23,** 185–191.

FABISZEWSKI, J. and WOJTUN, B. (1993): Peat-forming vegetation. The Maritime Antarctic Coastal Ecosystem of Admiralty Bay, ed. by S. RAKUSA-SUSZCZEWSKI. Warsaw, Dep. Antarctic Biol. Polish Academy of Science, 189–195.

FRENCH, D.D. and SMITH, V.R. (1986): Bacterial populations in soils of a Subantarctic island. Polar Biol., **6,** 75–82.

GRONDIN, A.E. and JOHANSEN, J.R. (1993): Microbial spatial heterogeneity in microbiotic crusts in Colorado National Monument. Great Basin Nat., **53,** 24–30.

HEATWOLE, H., SAENGER, P., SPAIN, A., KERRY, E. and DONELAN, J. (1989): Biotic and chemical characteristics of some soils from Wilkes Land, Antarctica. Antarct. Sci., **1,** 225–234.

KLUG, M.J. and TIEDJE, J.M. (1994): Responds of microbial communities to changing environmental conditions: Chemical and physical approaches. Trends in Microbial Ecology, ed. by R. GUERRERO and C. PEDROS-ALIO. Barcelona, Spanish Society for Microbiology, 371–378.

O'DONNELL, A.G., GOODFELLOW, M. and HAWKSWORTH D.L. (1994): Theoretical and practical aspects of the quantification of biodiversity among microorganisms. Philos. Trans. R. Soc. London B, **345,** 65–73.

OHTANI, S. and KANDA, H. (1987): Epiphytic algae on the moss community of Grimmia lawiana around Syowa Station, Antarctica. Proc. NIPR Symp. Polar Biol., **1,** 255–264.

OHTANI, S., AKIYAMA, M. and KANDA, H. (1991): Analysis of Antarctic soil algae by the direct observation using the contact slide method. Nankyoku Shiryô (Antarct. Rec.), **35,** 285–295.

OLECH, M. (1993): Lower plants. The Maritime Antarctic Coastal Ecosystem of Admiralty Bay, ed by S. RAKUSA-SUSZCZEWSKI. Warsaw, Dep. Antarctic Biol. Polish Academy of Science, 173–179.

PIEPENBURG, D. and PIATKOWSKI, U. (1992): A program for computer-aided analyses of ecological field data. Cabios, **8,** 587–590.

RAKUSA-SUSZCZEWSKI, S. and KRZYSZOWSKA, A. (1991): Assessment of the environmental impact of the "H. Arctowski" Polish Antarctic Station (Admiralty Bay, King George Island, South Shetland Islands). Pol. Polar Res., **12,** 105–121.

RAMSAY, A.J. (1983): Bacterial biomass in ornithogenic soils of Antarctica. Polar Biol., **1,** 221–225.

RAMSAY, A.J. and STANNARD, R.E. (1986): Numbers and viability of bacteria in ornithogenic soils of Antarctica. Polar Biol., **5,** 195–198.

ROSER, D.J., MELICK, D.R., LING, H.U. and SEPPELT, R.D. (1992): Polyol and sugar content of terrestrial plants from continental Antarctica. Antarct. Sci., **4,** 413–420.

ROSER, D.J., SEPPELT, R.D. and ASHBOLT, N. (1993): Microbiology of ornithogenic soils from the Windmill Islands, Budd Coast, continental Antarctica: Some observations on methods for measuring soil biomass in ornithogenic soils. Soil Biol. Biochem., **25,** 177–183.

WYNN-WILLIAMS, D.D. (1985): Photofading retardent for epifluorescence microscopy in soil micro-ecological studies. Soil Biol. Biochem., **17,** 739–746.

WYNN-WILLIAMS, D.D. (1988): Television image analysis of microbial communities in Antarctic fellfields. Polarforsching, **58,** 239–250.

WYNN-WILLIAMS, D.D. (1990): Microbial colonization processes in Antarctic fellfield soils –An experimantal overview. Proc. NIPR Symp. Polar Biol., **3,** 164–178.

WYNN-WILLIAMS, D.D. (1992): Direct quantification of microbial propagules and spores. BIOTAS Manual of Methods, ed. by D.D. WYNN-WILLIAMS. Cambridge, Scientific Committee on Antarctic, 34 p.

WYNN-WILLIAMS, D.D. (1993): Microbial processes and initial stabilization of fellfield soil. Primary Succession in Land, ed. by J. MILES and D.W.H. WALTON. Oxford, Blackwell, 17–32.

ZARZYCKI, K. (1993): Vascular plants and terrestrial biotopes. The Maritime Antarctic Coastal Ecosystem of

Admiralty Bay, ed by S. RAKUSA-SUSZCZEWSKI. Warsaw, Dep. Antarctic Biol. Polish Academy of Science, 181–187.

(Received January 30, 1995; Revised manuscript accepted September 19, 1995)