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PA 27

Microbial communities from terrestrial mineral soils from Livingston Island, maritime Antarctica

Introduction

Livingston Island, located at the tip of the Antarctic Peninsula (Figure 1), is characterised by an oceanic polar climate with temperatures above 0°C for 4 months per year and a mean annual precipitation between 400 and 500 mm. Under these conditions a soil formation can be observed and lichens, mosses and some higher plants are able to grow in this environment. We investigated the bacterial community structure of different mineral soil habitats by polymerase chain reaction (PCR) using a general bacterial primer set followed by denaturing gradient gel electrophoresis (DGGE) to get a first insight in the diversity of bacteria existing under these conditions.

Investigation Area

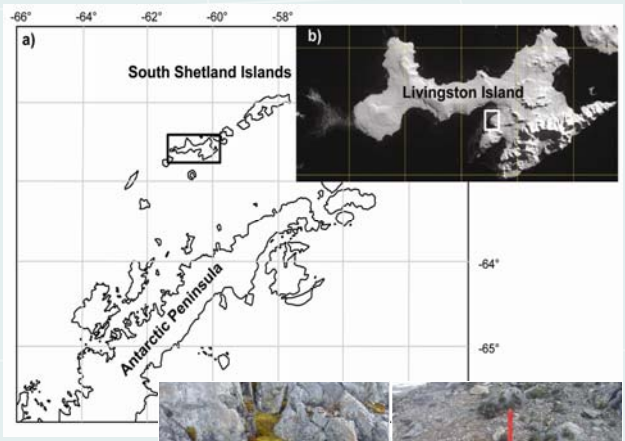
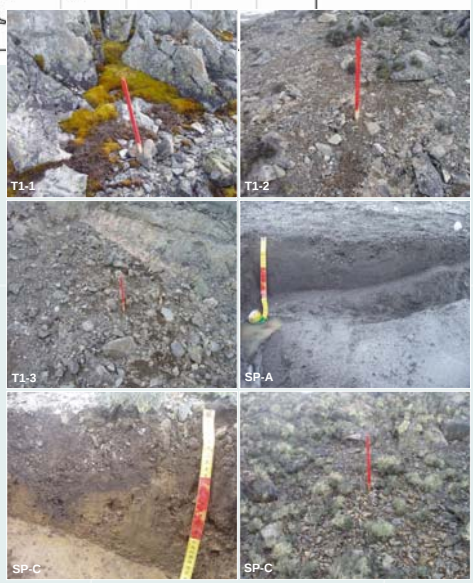


Fig. 1 Investigation area with sampling sites



Results

One transect and four separate soil profiles were sampled within walking distance of the Bulgarian station *St. Kliment Ohridski* (62°38`S/60°21`W) on Livingston Island. Two profiles were characterised by underlain permafrost. The investigated mineral soils showed mostly gravely sand texture (Table 1). Moisture content ranged from 2.6% up to 15.6%. Total carbon and total nitrogen content was low with <0.10 to 1.36% and <0.10% to 0.13%, respectively, except for the upper layers of profiles T1-1 and T1-4 that were covered by moss. Five profiles were investigated regarding the composition of phospholipid fatty acids (PLFA) and phospholipid ether lipids (PLEL). Almost all samples were dominated by straight chain saturated PLFAs (data not shown). Only the top layers of samples SP-A and SP-B showed a predominance of unsaturated PLFAs. PLELs were not detectable. DGGE pattern showed large varieties in the vertical profiles and between the different sites (Fig. 2). In total 183 sequences of ≥300 bp could be obtained from the nine soil profiles belonging to 87 operational taxonomic units (OTU; sequences sharing ≥97% similarity; Fig. 3).

Table 1: Soil geochemical and soil geospysical parameter

Site	Depth [cm]	Moisture [%]	Sand* [%]	Silt* [%]	Clay* [%]	Total C [%]	Total N [%]	pH	EC [µS/cm]	Number of culturable heterotrophs (g^{-1} dry soil)
T1-1	0-4	7.1	n.d.	n.d.	n.d.	26.50	0.84	4.81	n.d.	1.4×10^9
	4-7	4.7	73.9	20.4	5.7	2.22	0.20	6.04	88	7.0×10^8
	7-14	5.5	56.1	39.3	4.6	0.46	<0.10	6.10	40	4.9×10^6
T1-2	0-5	3.3	44.1	36.4	19.5	0.11	<0.10	7.22	38	6.2×10^4
	5-12	4.1	59.6	25.7	14.7	<0.10	<0.10	7.80	34	6.9×10^3
	12-24	3.9	49.1	31.4	19.5	<0.10	<0.10	7.82	37	6.9×10^4
T1-3	0-9	3.6	60.7	28.4	10.9	0.13	<0.10	7.58	49	3.5×10^4
	9-16	6.5	49.6	40.0	10.4	0.11	<0.10	7.16	34	1.4×10^5
	16-23	3.6	73.8	18.0	8.2	<0.10	<0.10	7.92	31	2.8×10^4
	23-30	8.3	50.5	38.0	11.5	<0.10	<0.10	7.23	31	3.7×10^4
T1-4	0-5	10.0	n.d.	n.d.	n.d.	9.34	0.32	5.97	n.d.	3.0×10^6
	5-8	9.2	75.4	15.7	8.9	2.31	0.19	6.77	112	7.3×10^5
	8-13	5.4	79.3	16.4	4.3	0.28	<0.10	7.53	48	1.4×10^4
	13-18	5.9	83.9	12.5	3.6	0.14	<0.10	7.83	39	2.5×10^4
T1-5	0-10	3.3	88.4	10.3	1.3	<0.10	<0.10	7.81	30	5.5×10^4
	10-20	3.8	86.3	12.1	1.6	<0.10	<0.10	8.01	28	1.4×10^4
	20-30	4.5	81.8	16.7	1.5	<0.10	<0.10	8.16	30	1.4×10^4
	30-40	5.0	84.5	14.3	1.2	<0.10	<0.10	7.94	30	2.8×10^4
	40-50	3.1	45.8	36.3	17.9	0.23	<0.10	8.45	100	3.4×10^4
SP-A	0-5	6.6	80.1	15.8	4.0	<0.10	<0.10	7.71	36	2.1×10^4
	5-10	7.0	81.6	15.0	3.4	<0.10	<0.10	8.04	31	4.3×10^4
	10-15	7.4	89.7	8.3	2.0	<0.10	<0.10	8.24	30	1.4×10^4
	15-20	9.9	92.4	6.4	1.2	<0.10	<0.10	8.61	39	2.2×10^4
	20-25	15.6	91.6	7.0	1.4	<0.10	<0.10	8.49	57	7.9×10^3
SP-B	0-5	2.6	93.0	5.6	1.4	0.15	<0.10	7.48	42	4.1×10^4
	5-10	9.9	57.5	39.5	3.0	0.19	<0.10	7.69	34	3.7×10^4
	10-15	7.8	46.7	50.2	3.1	0.11	<0.10	7.83	34	1.1×10^5
	15-20	10.3	41.3	56.4	2.4	<0.10	<0.10	7.78	33	1.5×10^4
	20-25	6.4	31.4	64.1	4.6	0.10	<0.10	7.84	37	7.1×10^3
	25-30	11.1	51.0	45.1	3.9	0.14	<0.10	8.02	41	n.d.
	30-35	10.3	36.9	59.6	3.6	<0.10	<0.10	7.91	37	1.5×10^4
SP-C	0-10	2.7	69.1	24.2	6.7	0.21	<0.10	7.07	53	2.1×10^4
	10-20	5.6	41.3	50.8	7.9	0.38	<0.10	7.48	44	2.0×10^4
	20-30	5.3	45.0	49.0	6.0	0.17	<0.10	7.49	35	1.4×10^4
SP-D	0-5	4.5	75.6	18.9	5.5	0.45	<0.10	7.26	65	8.4×10^4
	5-10	5.1	71.9	20.1	8.1	0.48	<0.10	7.41	74	7.0×10^4
	10-15	6.2	12.0	71.2	16.8	1.21	0.12	7.37	91	2.8×10^4
	15-20	5.4	42.0	47.3	10.7	1.36	0.13	7.24	101	7.0×10^3

* part of the grain size fraction < 2mm, n.d. - not determined

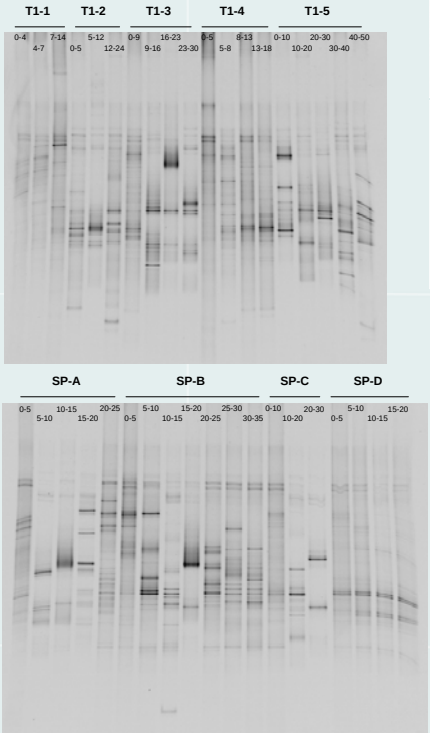


Fig. 2 DGGE profiles of 16S rRNA gene amplicons from different mineral soil profiles from Livingston Island. T1-1 to T1-5 represent five profiles of the investigated transect, whereas SP-A, SP-B, SP-C and SP-D stand for a single profile. Numbers in the DGGE pictures indicate the sample depth.

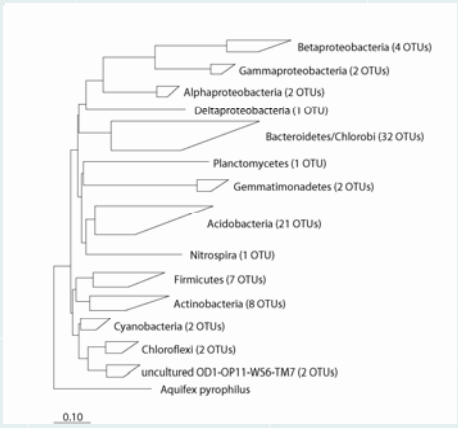


Fig. 3 Simplified phylogenetic tree showing affiliation of amplified 16S rRNA gene fragments and the number of OTUs belonging to a certain bacterial group

Conclusions

DGGE pictures and phylogenetic investigations showed a distinct diversity for maritime Antarctic mineral soils. Main influence on heterotrophic microbial growth and activity in low-nutrient habitats is probably the availability of organic compounds when a plant cover is nonexistent. It is conceivable that the ways of C and N cycling in cold antarctic habitats are short, so that no or only slow accumulation of organic matter is possible.

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