

Supplementary Materials

Lanthanide-dependent methanol metabolism of *Proteobacteria*-dominated community in light lanthanide-rich deep environment

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Table S1. Detected genera that Semrau et al. (2010) listed as aerobic methanotrophs.

Phylum	Family	Genus	avg(genus)	Species	reads ion21	reads ion22	reads ion23	% reads21	% reads22	% reads23	AVG	SD
Gammaproteobacteria	Methylococcaceae	Methylobacter	0.4085	<i>Candidatus Methylobacter oryzae</i>	1181	268	53	0.0546	0.0080	0.0335	0.0321	0.0233
				<i>Methylobacter luteus</i>	1974	348	62	0.0913	0.0105	0.0392	0.0470	0.0410
				<i>Methylobacter marinus</i>	390	49	16	0.0180	0.0015	0.0101	0.0099	0.0083
				<i>Methylobacter</i> sp. BBA5.1	5689	574	143	0.2631	0.0172	0.0904	0.1236	0.1263
				<i>Methylobacter tundripaludum</i>	4382	841	153	0.2027	0.0253	0.0967	0.1082	0.0893
				<i>Methylobacter whittenburyi</i>	222	36	7	0.0103	0.0011	0.0044	0.0053	0.0046
				unclassified <i>Methylobacter</i>	3434	726	106	0.1588	0.0218	0.0670	0.0825	0.0698
		Methylococcus	0.0113	<i>Methylococcus capsulatus</i>	305	111	26	0.0141	0.0033	0.0164	0.0113	0.0070
		Methylocaldum	0.0617	<i>Methylocaldum marinum</i>	607	146	21	0.0281	0.0044	0.0133	0.0152	0.0120
				<i>Methylocaldum</i> sp. 0917	60	13	5	0.0028	0.0004	0.0032	0.0021	0.0015
				<i>Methylocaldum</i> sp. 14B	67	22	4	0.0031	0.0007	0.0025	0.0021	0.0013
				<i>Methylocaldum</i> sp. BRCS4	129	11	6	0.0060	0.0003	0.0038	0.0034	0.0028
				<i>Methylocaldum</i> sp. SAD2	12	8	1	0.0006	0.0002	0.0006	0.0005	0.0002

Phylum	Family	Genus	avg(genus)	Species	reads ion21	reads ion22	reads ion23	% reads21	% reads22	% reads23	AVG	SD
				<i>Methylocaldum szegediense</i>	304	98	12	0.0141	0.0029	0.0076	0.0082	0.0056
				<i>unclassified Methylocaldum</i>	1029	260	56	0.0476	0.0078	0.0354	0.0303	0.0204
		<i>Methylohalobius</i>	0.0067	<i>Methylohalobius crimeensis</i>	227	86	11	0.0105	0.0026	0.0070	0.0067	0.0040
		<i>Methylomicrobium</i>	0.2300	<i>Methylomicrobium agile</i>	5450	929	176	0.2521	0.0279	0.1112	0.1304	0.1133
				<i>Methylomicrobium alcaliphilum</i>	184	56	13	0.0085	0.0017	0.0082	0.0061	0.0039
				<i>Methylomicrobium buryatense</i>	513	104	21	0.0237	0.0031	0.0133	0.0134	0.0103
				<i>Methylomicrobium kenyense</i>	696	141	35	0.0322	0.0042	0.0221	0.0195	0.0142
				<i>Methylomicrobium</i> sp. wino1	1386	237	36	0.0641	0.0071	0.0227	0.0313	0.0294
				<i>unclassified Methylomicrobium</i>	1117	274	44	0.0517	0.0082	0.0278	0.0292	0.0218
		<i>Methylomonas</i>	2.5868	<i>Methylomonas denitrificans</i>	2	2	0	0.0001	0.0001	0.0000	0.0001	0.0000
				<i>Methylomonas koyamae</i>	16454	4345	2711	0.7610	0.1305	1.7131	0.8682	0.7967
				<i>Methylomonas lenta</i>	1999	1048	148	0.0925	0.0315	0.0935	0.0725	0.0355
				<i>Methylomonas methanica</i>	10661	8269	902	0.4931	0.2484	0.5700	0.4371	0.1679
				<i>Methylomonas</i> sp. 11b	1201	284	59	0.0555	0.0085	0.0373	0.0338	0.0237
				<i>Methylomonas</i> sp. DH-1	231	76	28	0.0107	0.0023	0.0177	0.0102	0.0077
				<i>Methylomonas</i> sp. GJ1	1213	656	100	0.0561	0.0197	0.0632	0.0463	0.0233
				<i>Methylomonas</i> sp. Kb3	500	95	26	0.0231	0.0029	0.0164	0.0141	0.0103
				<i>Methylomonas</i> sp. LW13	268	68	22	0.0124	0.0020	0.0139	0.0094	0.0065
				<i>Methylomonas</i> sp. LWB	1643	277	98	0.0760	0.0083	0.0619	0.0487	0.0357
				<i>Methylomonas</i> sp. MK1	1754	371	73	0.0811	0.0111	0.0461	0.0461	0.0350
				<i>unclassified Methylomonas</i>	26204	8985	2403	1.2120	0.2699	1.5184	1.0001	0.6507
		<i>Methylosoma</i>	not found	n/a	n/a*	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		<i>Methylosarcina</i>	5.7403	<i>Methylosarcina fibrata</i>	253415	39968	5971	11.7207	1.2005	3.7730	5.5648	5.4842
				<i>Methylosarcina lacus</i>	4752	828	132	0.2198	0.0249	0.0834	0.1094	0.1000
				<i>unclassified Methylosarcina</i>	3002	496	71	0.1388	0.0149	0.0449	0.0662	0.0647
		<i>Methylosphaera</i>	not found	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		<i>Methylothermus</i>	not found	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		<i>Crenothrix</i>	0.0435	<i>Crenothrix polyspora</i>	1592	396	71	0.0736	0.0119	0.0449	0.0435	0.0309

Phylum	Family	Genus	avg(genus)	Species	reads ion21	reads ion22	reads ion23	% reads21	% reads22	% reads23	AVG	SD
		<i>Clonothrix</i>	not found	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
<i>Alphaproteobacteria</i>	<i>Methylocystaceae</i>	<i>Methylosinus</i>	0.0083	<i>Methylosinus</i> sp. C49	12	7	1	0.0006	0.0002	0.0006	0.0005	0.0002
				<i>Methylosinus</i> sp. Ce-a6	16	23	1	0.0007	0.0007	0.0006	0.0007	0.0001
				<i>Methylosinus</i> sp. LW3	11	9	1	0.0005	0.0003	0.0006	0.0005	0.0002
				<i>Methylosinus</i> sp. LW4	10	13	2	0.0005	0.0004	0.0013	0.0007	0.0005
				<i>Methylosinus</i> sp. PW1	32	12	4	0.0015	0.0004	0.0025	0.0015	0.0011
				<i>Methylosinus</i> sp. R-45379	17	1	0	0.0008	0.0000	0.0000	0.0003	0.0004
				<i>Methylosinus sporium</i>	28	15	0	0.0013	0.0005	0.0000	0.0006	0.0007
				<i>Methylosinus trichosporium</i>	0	3	0	0.0000	0.0001	0.0000	0.0000	0.0001
				unclassified <i>Methylosinus</i>	85	64	8	0.0039	0.0019	0.0051	0.0036	0.0016
		<i>Methylocystis</i>	0.0447	<i>Methylocystis bryophila</i>	28	34	7	0.0013	0.0010	0.0044	0.0022	0.0019
				<i>Methylocystis heyeri</i>	53	38	4	0.0025	0.0011	0.0025	0.0020	0.0008
				<i>Methylocystis hirsuta</i>	59	41	6	0.0027	0.0012	0.0038	0.0026	0.0013
				<i>Methylocystis parvus</i>	84	81	7	0.0039	0.0024	0.0044	0.0036	0.0010
				<i>Methylocystis rosea</i>	85	112	6	0.0039	0.0034	0.0038	0.0037	0.0003
				<i>Methylocystis</i> sp. ATCC 49242	89	87	4	0.0041	0.0026	0.0025	0.0031	0.0009
				<i>Methylocystis</i> sp. B8	104	152	5	0.0048	0.0046	0.0032	0.0042	0.0009
				<i>Methylocystis</i> sp. MitZ-2018	22	33	6	0.0010	0.0010	0.0038	0.0019	0.0016
				<i>Methylocystis</i> sp. SB2	11	6	1	0.0005	0.0002	0.0006	0.0004	0.0002
				<i>Methylocystis</i> sp. SC2	26	49	2	0.0012	0.0015	0.0013	0.0013	0.0001
				unclassified <i>Methylocystis</i>	337	551	42	0.0156	0.0166	0.0265	0.0196	0.0061
	<i>Beijerinckaceae</i>	<i>Methylocapsa</i>	0.0073	<i>Methylocapsa acidiphila</i>	28	39	3	0.0013	0.0012	0.0019	0.0015	0.0004
				<i>Methylocapsa aurea</i>	40	36	5	0.0019	0.0011	0.0032	0.0020	0.0011
				<i>Methylocapsa palsarum</i>	41	26	1	0.0019	0.0008	0.0006	0.0011	0.0007
				<i>Methylocapsa</i> sp. S129	66	68	3	0.0031	0.0020	0.0019	0.0023	0.0006
				unclassified <i>Methylocapsa</i>	8	5	1	0.0004	0.0002	0.0006	0.0004	0.0002
		<i>Methylocella</i>	0.0062	<i>Methylocella silvestris</i>	105	82	10	0.0049	0.0025	0.0063	0.0045	0.0019
				<i>Methylocella tundrae</i>	29	53	2	0.0013	0.0016	0.0013	0.0014	0.0002
				unclassified <i>Methylocella</i>	2	1	1	0.0001	0.0000	0.0006	0.0003	0.0003
<i>Verrucomicrobia</i>	<i>Methylacidiphilaceae</i>	<i>Methylacidiphilum</i>	0.0078	<i>Methylacidiphilum fumariolicum</i>	10	9	3	0.0005	0.0003	0.0019	0.0009	0.0009

Phylum	Family	Genus	avg(genus)	Species	reads ion21	reads ion22	reads ion23	% reads21	% reads22	% reads23	AVG	SD
				<i>Methylacidiphilum infernorum</i>	22	35	5	0.0010	0.0011	0.0032	0.0017	0.0012
				<i>Methylacidiphilum kamchatkense</i>	10	5	0	0.0005	0.0002	0.0000	0.0002	0.0002
				<i>Methylacidiphilum</i> sp. Phi	30	22	3	0.0014	0.0007	0.0019	0.0013	0.0006
				<i>Methylacidiphilum</i> sp. Yel	13	6	0	0.0006	0.0002	0.0000	0.0003	0.0003
				unclassified <i>Methylacidiphilum</i>	85	81	6	0.0039	0.0024	0.0038	0.0034	0.0008

* n/a - not applicable

Table S2. Methane monooxygenase sequences detected in the metaproteome and metagenome of the studied microbial community.

NCBI sequence no.	Description	Genus/Species	Order (Class)
Metagenomic data			
WP_202053531	methane/ammonia monooxygenase subunit A [EC:1.14.18.3 1.14.99.39]	Methyломicrobium sp. RS1	Methylococcales (Gammaproteobacteria)
WP_020564882	methane/ammonia monooxygenase subunit B	Methylosarcina fibrata	
WP_202053530	methane/ammonia monooxygenase subunit B	Methyломicrobium sp. RS1	
WP_150047786	methane/ammonia monooxygenase subunit B	Methylomonas rhizoryzae	
WP_192392143	methane/ammonia monooxygenase subunit B	Methylomonas sp. EbB	
WP_020564880	methane/ammonia monooxygenase subunit C	Methylosarcina fibrata	
WP_026223479	methane/ammonia monooxygenase subunit C	Methylosarcina fibrata	
Metaproteomic data			
WP_014892305	methane monooxygenase	Methylocystis sp. SC2	Hyphomicrobiales (Alphaproteobacteria)
WP_018408664	MULTISPECIES: methane monooxygenase	Methylocystis	Methylococcales (Gammaproteobacteria)
WP_013817027	methane monooxygenase	Methylomonas methanica	
WP_018408664	methane monooxygenase	Methylomonas sp. MK1	
WP_020564882	methane monooxygenase	Methylosarcina fibrata	
BAE86886	methane monooxygenase protein B	Methyломicrobium japonense	
BAH22841	methane monooxygenase protein C	Methylomarinum vadi	
WP_064028764	methane monooxygenase/ammonia monooxygenase subunit B	Methylomonas koyamae	
WP_064028760	methane monooxygenase/ammonia monooxygenase subunit C	Methylomonas koyamae	
BAJ17642	particulate methane monooxygenase B-subunit	Methylovulum miyakonense HT12	
BAJ17640	particulate methane monooxygenase G-subunit	Methylovulum miyakonense HT12	
ACE95894	particulate methane monooxygenase subunit A	Methylomonas methanica	
WP_010961049	particulate methane monooxygenase subunit alpha	Methylococcus capsulatus	

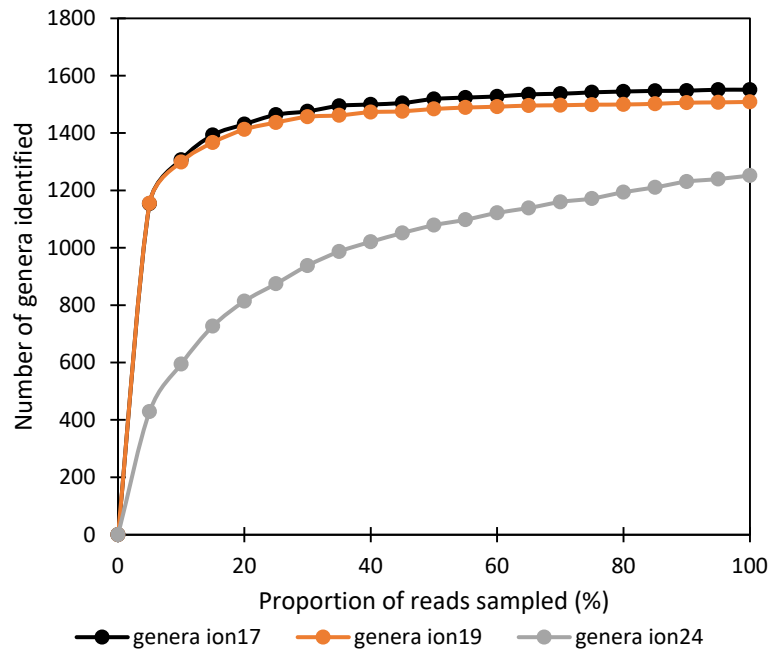


Figure S1. Rarefaction curves representing the relationship between the number of taxa as a function of sequencing depth (proportion of reads sampled). Rarefaction analysis showed that sequencing saturation was achieved almost for all samples.