

Supplementary Material for

Community structure and abundance of archaea in a *Zostera marina* meadow: A comparison between seagrass-colonized and bare sediment sites

Pengfei Zheng^{1,2}, Chuantao Wang³, Xiaoli Zhang^{1*}, Jun Gong^{1, 4, 5*}

¹CAS Key Laboratory of Coastal Environmental Processes and Ecological Remediation, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China.

²University of Chinese Academy of Sciences, Beijing 100049, China.

³Shandong Oriental Ocean Sci-tech Co., Ltd, Yantai 264003, China.

⁴Laboratory of Microbial Ecology and Matter Cycles, School of Marine Sciences, Sun Yat-Sen University, Zhuhai 519082, China.

⁵Southern Marine Science and Engineering Guangdong Laboratory (Zhuhai), Zhuhai, China

Corresponding author

Xiaoli Zhang, Email: xlzhang@yic.ac.cn

Jun Gong, Email: gongj27@mail.sysu.edu.cn

Contents of this file

Figures S1 and S2

Tables S1 and Tables S2

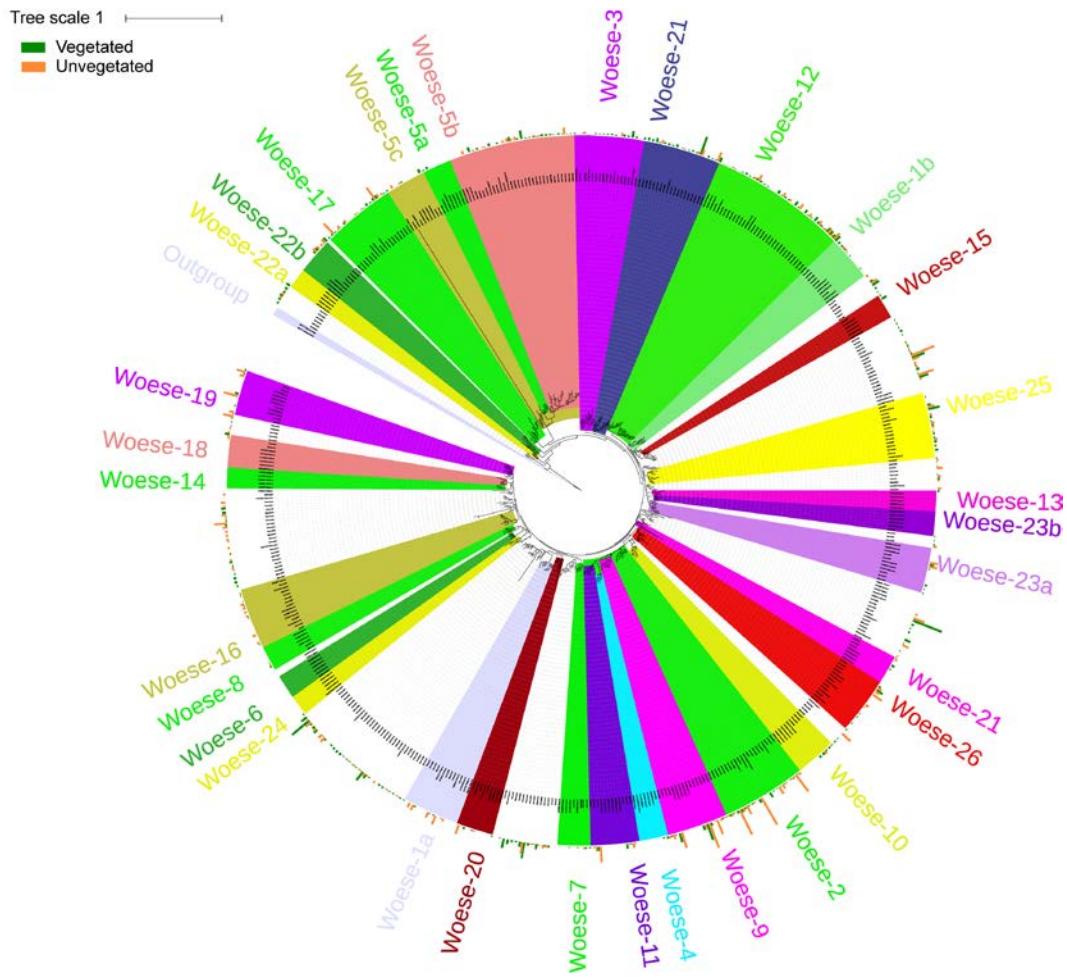


Figure S1 The phylogenetic maximum-likelihood (ML) tree was constructed for all *Woesearchaeota* 16S rRNA gene sequences obtained in the study with bacterial 16S rRNA gene sequences as the outgroup. Sequences for typical *Woesearchaeota* subclades according to the nomenclature promoted by Liu et al. (2018) are used as major references for constructing the phylogenetic tree. The ML tree was built with the “FastTree” program and edited with the online tool iTOL (<http://itol.embl.de/>)

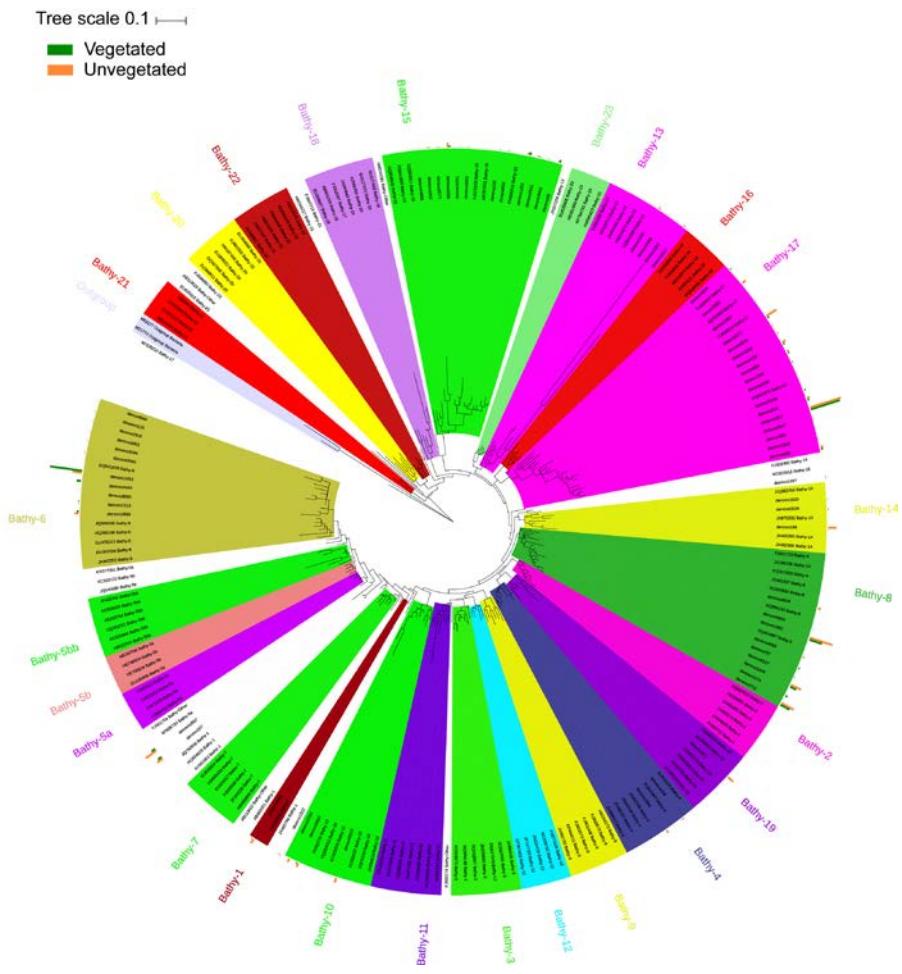


Figure S2 The phylogenetic maximum-likelihood (ML) tree was built for all *Bathyarchaeota* 16S rRNA gene sequences obtained in this study with bacterial 16S rRNA gene sequences as the outgroup. Sequences for typical *Bathyarchaeota* subclades according to the nomenclature promoted by Zhou et al. (2018) are used as major references for constructing the phylogenetic tree. The ML tree was built with the “FastTree” program and edited with the online tool iTOL (<http://itol.embl.de/>)

Table S1 Summary of archaeal sequence information and alpha diversity in all sediment samples

Sample ID	Sequence information				Alpha diversity			
	Raw seqs	Quality seqs	After discarding chimera seqs	After discarding singleton seqs	OTU Richness	Chao1	Shannon	Simpson
V1	28136	21783	14139	6326	141	296.88	6.39	0.98
V2	22951	10501	9010	8343	167	353.84	6.96	0.99
V3	14610	11770	6839	6326	152	343.40	6.62	0.98
U1	13293	5402	4840	4596	137	198.72	6.74	0.99
U2	7618	3643	3386	3285	135	211.68	6.52	0.98
U3	14028	5843	5305	5046	156	311.70	6.82	0.99

Table S2 Comparison of the relative proportions and 16S rRNA gene copy numbers of archaeal lineages based on SILVA (v. 128) between the vegetated and unvegetated sediments. The pairwise differences were examined using *t*-tests (n=3)^a

Taxonomy	% Relative proportion			Copy numbers (mean ± SE)		
	(mean ± SE)			(x10 ⁶ copies g ⁻¹ sediment)		
	Unvegetated	Vegetated	P	Unvegetated	Vegetated	P
Woesearchaeota	45.45±0.98	39.34±7.72	0.556	5.31±1.13	11.98±2.75	0.141
Woese-10	0.15±0.12	0.55±0.07	0.076	0.01±0.01	0.16±0.03	0.014
Woese-11	2.34±0.81	3.53±1.43	0.586	0.22±0.07	1.08±0.42	0.173
Woese-12	2.03±0.57	3.19±0.58	0.311	0.27±0.12	1.01±0.31	0.139
Woese-13	0.41±0.17	1.26±0.32	0.130	0.04±0.02	0.36±0.07	0.027
Woese-14	0.36±0.04	0.99±0.52	0.385	0.04±0.01	0.35±0.21	0.305
Woese-15	0±0	0.35±0.24	0.297	0±0	0.13±0.09	0.315
Woese-16	0.95±0.1	0.28±0.23	0.092	0.10±0.01	0.08±0.07	0.796
Woese-17	1.35±0.21	0.58±0.18	0.090	0.16±0.04	0.15±0.04	0.877
Woese-19	2.15±0.6	0.67±0.37	0.160	0.24±0.07	0.21±0.11	0.834
Woese-1a	1.59±0.32	0.59±0.15	0.082	0.2±0.07	0.18±0.05	0.808
Woese-1b	0.58±0.26	0.35±0.13	0.551	0.08±0.04	0.10±0.03	0.877
Woese-2	9.24±1.87	4.35±1.27	0.153	0.96±0.05	1.31±0.39	0.499
Woese-20	2.26±0.14	0.80±0.30	0.023	0.27±0.07	0.25±0.09	0.912
Woese-21	0±0	0.26±0.03	0.003	0±0	0.07±0	0
Woese-22a	0±0	0.04±0.03	0.374	0±0	0.01±0.01	0.374
Woese-23a	0±0	0.09±0.07	0.374	0±0	0.03±0.03	0.374
Woese-24	0±0	0.09±0.07	0.374	0±0	0.03±0.03	0.374
Woese-25	0.90±0.080	1.05±0.14	0.510	0.11±0.03	0.33±0.09	0.125
Woese-26	0.75±0.30	0.40±0.14	0.435	0.10±0.06	0.13±0.06	0.798
Woese-3	0.11±0.09	0.55±0.03	0.018	0.01±0.01	0.17±0.03	0.011

Woese-4	0.07±0.06	0.13±0.11	0.709	0.01±0.01	0.05±0.04	0.445
Woese-5a	0.12±0.1	0.31±0.26	0.599	0.02±0.02	0.07±0.06	0.537
Woese-5b	2.11±1.39	2.23±0.46	0.951	0.34±0.24	0.67±0.15	0.395
Woese-7	0.18±0.15	0.30±0.07	0.599	0.02±0.02	0.10±0.03	0.167
Woese-8	1.60±0.06	1.48±0.63	0.889	0.18±0.03	0.45±0.18	0.301
Woese-9	5.36±0.32	3.63±1.70	0.460	0.63±0.15	1.11±0.49	0.482
Woese-Other	10.84±0.51	11.31±1.83	0.851	1.29±0.30	3.40±0.66	0.077
<i>Bathyarchaeota</i>	15.44±3.87	26.17±5.40	0.258	1.61±0.33	7.43±1.13	0.016
Bathy-1	1.01±0.28	1.25±0.23	0.609	0.1±0.02	0.39±0.12	0.125
Bathy-10	0.44±0.36	0.04±0.03	0.417	0.04±0.04	0.01±0.01	0.477
Bathy-13	0.07±0.06	0.06±0.03	0.908	0.01±0.01	0.02±0.01	0.430
Bathy-14	1.67±0.70	1.16±0.43	0.635	0.22±0.09	0.39±0.19	0.552
Bathy-15	0.75±0.34	1.77±0.34	0.160	0.07±0.03	0.49±0.04	0.002
Bathy-17	4.63±1.69	7.10±2.66	0.557	0.46±0.16	1.93±0.55	0.103
Bathy-18	0±0	0.13±0.03	0.035	0±0	0.04±0.01	0.005
Bathy-19	0.36±0.30	0±0	0.374	0.04±0.03	0±0	0.374
Bathy-23	0.19±0.15	0±0	0.374	0.01±0.01	0±0	0.374
Bathy-4	0.15±0.12	0±0	0.374	0.01±0.01	0±0	0.374
Bathy-6	1.80±0.47	8.15±1.16	0.014	0.21±0.07	2.41±0.45	0.017
Bathy-8	4.30±1.16	6.48±1.63	0.423	0.42±0.08	1.75±0.22	0.010
Bathy-Other	0.07±0.06	0.02±0.02	0.525	0.01±0.01	0±0	0.751
<i>Thaumarchaeota</i>	21.46±1.35	12.6±1.23	0.017	2.51±0.56	3.89±0.88	0.338
Group C3	6.59±0.62	8.67±0.77	0.16	0.74±0.11	2.61±0.48	0.036
Marine Benthic Group A	0±0	0.02±0.02	0.374	0±0	0±0	0.374
Marine Group I	8.04±2.16	0.99±0.40	0.059	0.80±0.08	0.33±0.14	0.072
Soil Crenarchaeotic Group (SCG)	6.84±2.73	2.80±0.75	0.309	0.97±0.54	0.92±0.32	0.951
South African Gold Mine Gp 1 (SAGMCG-1)	0±0	0.04±0.04	0.374	0±0	0.02±0.01	0.374
<i>Euryarchaeota</i>	10.81±2.29	13.32±1.33	0.482	1.4±0.52	4.04±0.83	0.093
<i>Halobacteria</i>	0.37±0.15	0.08±0.02	0.192	0.05±0.03	0.02±0.01	0.491
<i>Methanobacteria</i>	3.57±1.67	1.42±0.28	0.358	0.52±0.32	0.45±0.14	0.878
<i>Methanomicrobia</i>	0.44±0.27	0.37±0.14	0.86	0.07±0.05	0.11±0.04	0.639
<i>Thermoplasmata</i>	6.42±1.32	11.45±1.42	0.101	0.75±0.18	3.45±0.73	0.043
<i>Aenigmarchaeota</i>	3.73±1.16	0.89±0.37	0.13	0.41±0.12	0.26±0.11	0.476
Deep Sea Euryarchaeotic Group (DSEG)	3.73±1.16	0.89±0.37	0.13	0.41±0.12	0.26±0.11	0.476

<i>Lokiarchaeota</i>		1.86±0.56	3.33±1.24	0.427	0.21±0.07	0.91±0.27	0.108	
Marine	Hydrothermal	Vent	0.44±0.19	1.64±0.31	0.055	0.04±0.02	0.47±0.06	0.006
Group (MHVG)								
Miscellaneous	Euryarchaeotic		0.26±0.13	0.68±0.22	0.255	0.02±0.01	0.18±0.04	0.03
Group (MEG)								
<i>Altarchaeales</i>		0.16±0.09	0.04±0.04	0.387	0.02±0.02	0.02±0.01	0.791	
Ancient	Archaeal	Group	0±0	1.19±0.51	0.132	0±0	0.38±0.19	0.188
(AAG)								
AK8		0.07±0.06	0.11±0.07	0.73	0.01±0.01	0.03±0.01	0.327	
<i>Diapherotrites</i>		0.07±0.06	0.21±0.11	0.41	0.01±0.01	0.06±0.03	0.242	
WSA2		0.24±0.20	0.16±0.08	0.772	0.04±0.03	0.05±0.02	0.902	
20a-9		0.24±0.20	0.16±0.08	0.772	0.04±0.03	0.05±0.02	0.902	
Unclassified Archaea		0±0	0.33±0.13	0.117	0±0	0.1±0.04	0.135	

^a Significant differences ($P < 0.05$) are highlighted in bold.