Stratification of Microbial Community in Marine Sediments of the Ross Sea, Antarctica

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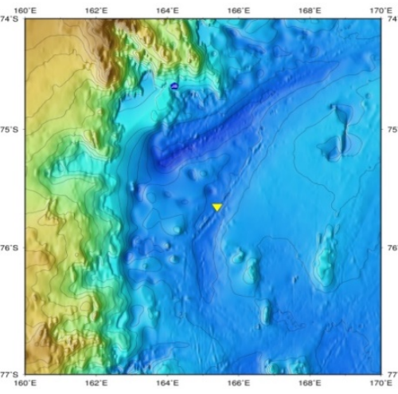
Introduction

The deep subseafloor biosphere is the least-understood habitat on Earth, even though the amount of microbial biomass therein plays important roles in the biogeochemical cycles and remineralization of organic materials. In this study, microbial community of 21 sediment horizons from one gravity core (approximately 4 m) collected in the Ross Sea was profiled by pyrosequencing. Distinct stratification in the microbial community within the gravity core was observed. Bacterial community showed distinctive stratification from *Proteobacteria*, *Planctomycetes*, *Bacteroidetes*, *Acidobacteria*, and *Chlorobi* in the aerobic upper sediment column towards OP9, *Chloroflexi*, and *Actinobacteria* in anaerobic sediment horizons. Interestingly, uncultured candidate phylum OP9 was predominant from 40 cm below seafloor composing up to 54.2%, indicating initial constraints for their microbial habitat preferences. Archaea also showed a dramatic shift in community composition at the oxic-anoxic transition zone as was the case for bacteria. *Crenarchaeota* was the most dominant archaeal phylum throughout the sediment. However, relative abundance of *Crenarchaeota* classes varied considerably along the depth. Eukaryotic community showed *Stramenopiles* and unassigned group to any phyla were dominant throughout the sediment. However, relative abundance of *Alveolata* and *Metazoa* showed significant decrease along sediment depth, especially across the oxic–anoxic transition.

Materials & Methods

Sampling

- **Location:** 75° 39.5684’ S
  165° 23.8382’ E
- **Date:** January 15, 2012
- **Collection:** Gravity core



- gDNA extraction
- PCR
- Pyrosequencing
  - Bacteria: 27F/519R
  - Archaea: ArcF/ArcR
  - Eukaryotes: LSU

- Nutrient analysis
  - XRF scanning

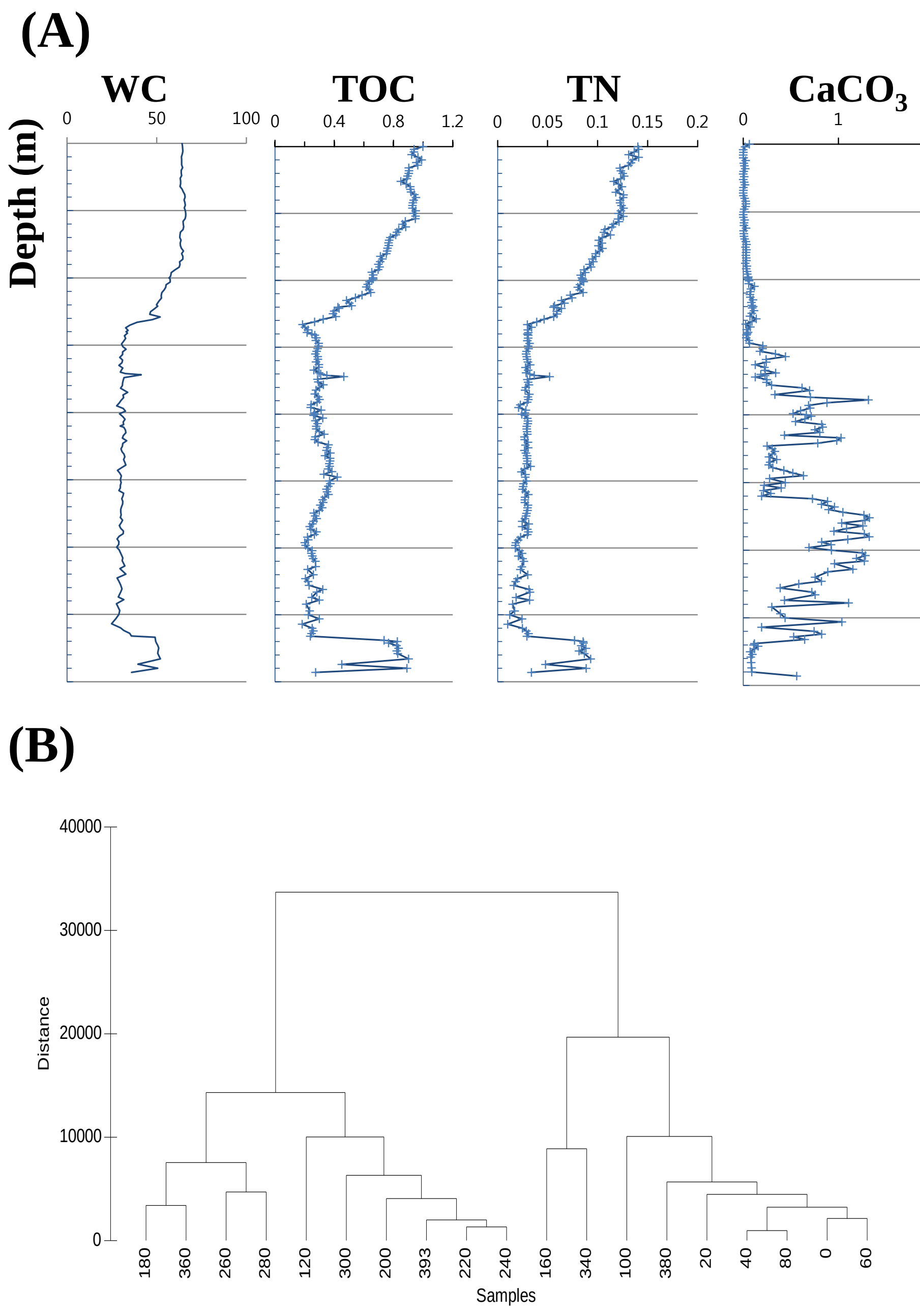
- Trimming
- Clustering
- Chimera check
- Taxonomic assignment
  - PyroTrimmer (Oh et al., 2012)
  - Clustom (Hwang et al., 2013)
  - UCHIME (Edgar et al., 2011)
  - EzTaxon-e (Kim et al., 2012)

Statistical analysis

- PCA: Primer 6
- Pearson correlation: R

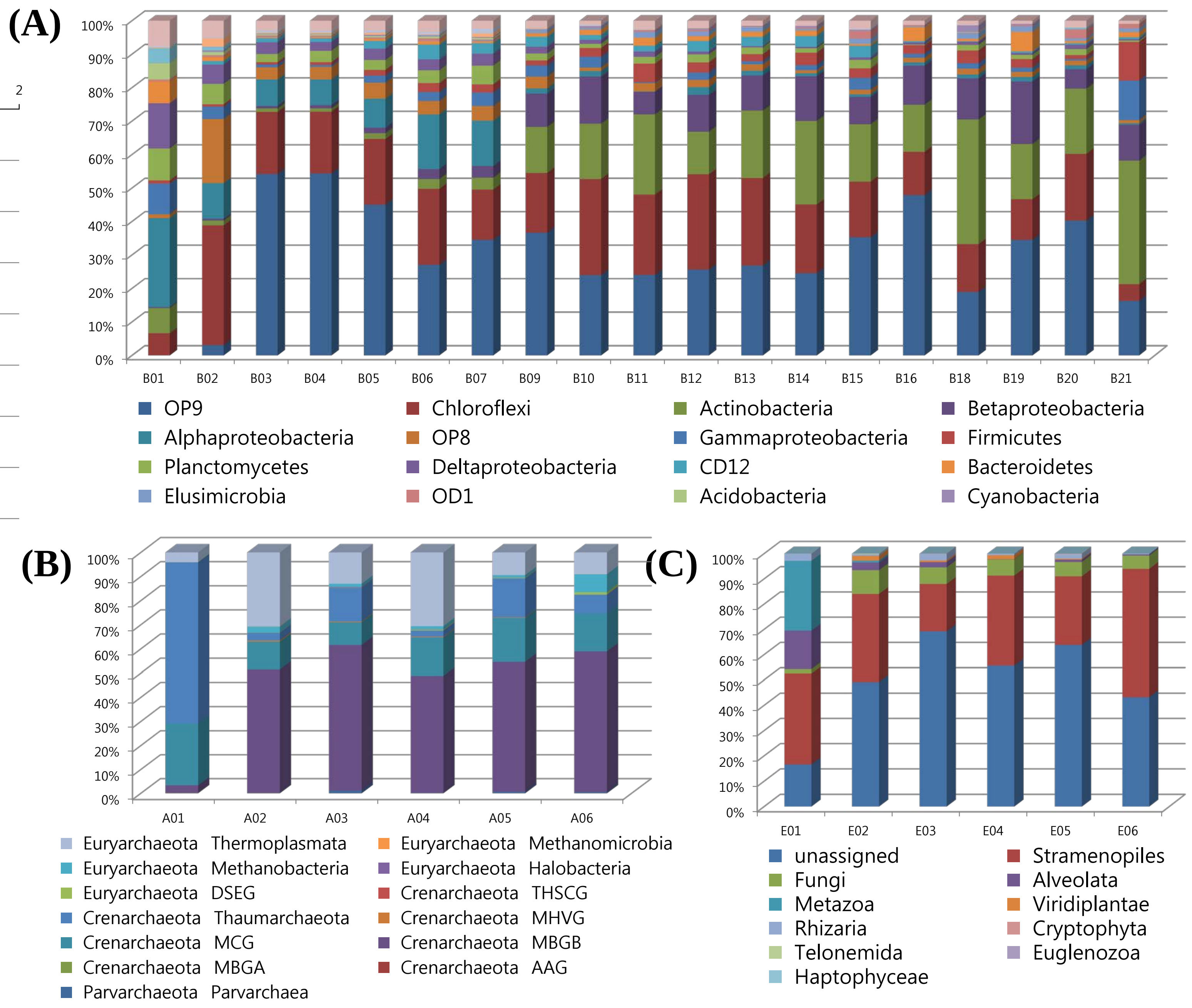
Results

1. Nutrients

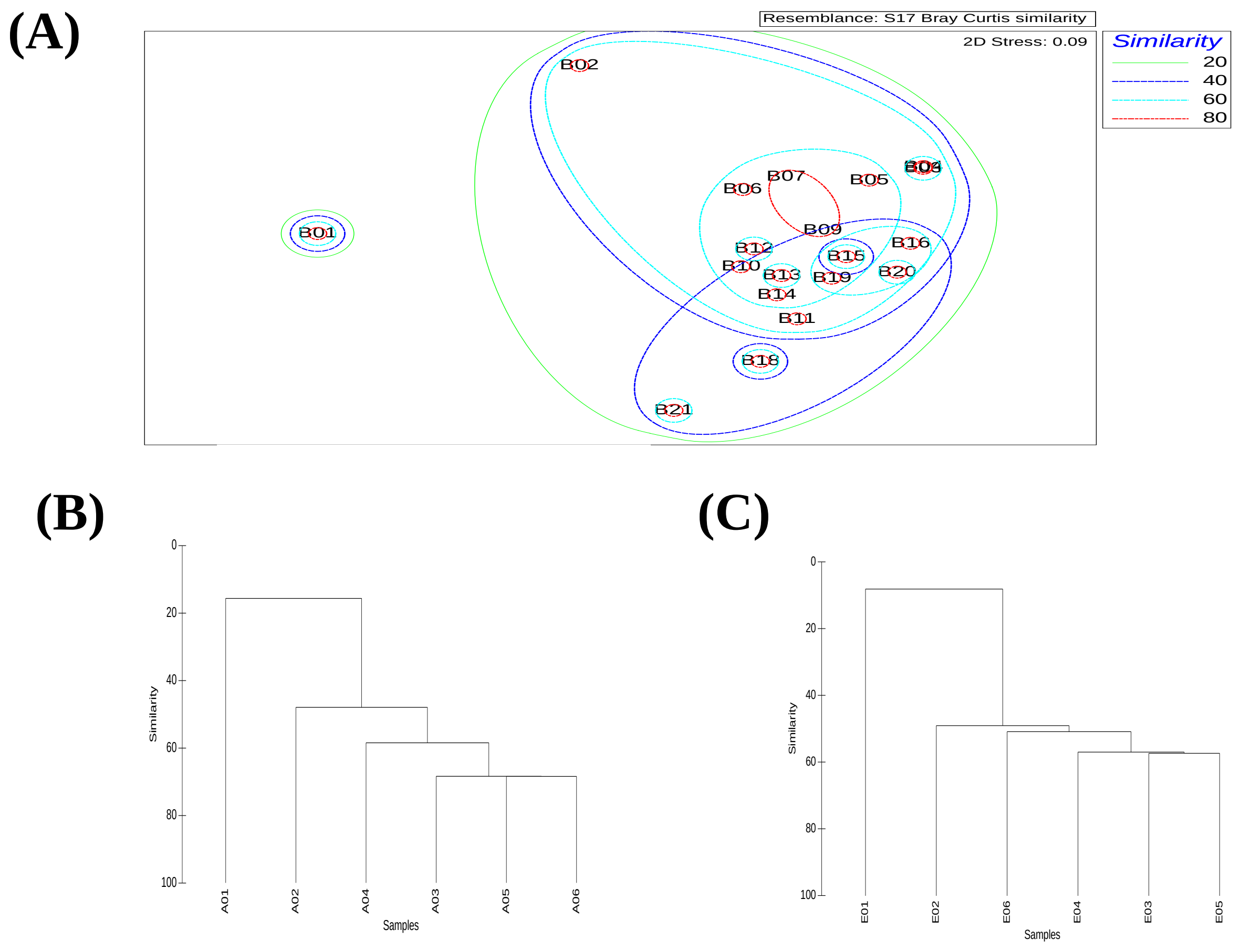


▲ Fig. 1 Nutrients of core (A) and similarities of samples by environmental variables (B)

2. Microbial composition and similarities between samples



▲ Fig. 2 Composition of microbial communities by pyrosequencing
Bacterial communities (A),
Archaeal communities (B),
Eukaryotic communities (C)



▲ Fig. 3 Similarities of samples by bacterial composition
Bacterial communities (A),
Archaeal communities (B),
Eukaryotic communities (C)

3. Correlation

Phylum	B01	B02	B03	B04	B05	B06	B07	B09	B10	B11	B12	B13	B14	B15	B16	B18	B19	B20	B21	r	p-value
Actinobacteria	7.51	1.42	1.05	1.01	1.71	2.94	3.59	13.77	16.54	23.99	12.71	20.16	24.97	17.15	14.07	37.26	16.48	19.49	36.92	0.82	1.66E-05
Betaproteobacteria	0.26	0.55	0.72	0.92	1.64	2.97	3.47	9.93	14.11	6.73	11.00	10.51	13.36	8.15	11.69	12.27	18.71	5.82	10.71	0.78	8.80E-05
AC1	0.00	0.00	0.08	0.00	0.00	0.00	0.00	0.00	0.12	0.29	0.34	0.11	0.12	0.41	0.59	0.14	0.35	0.68	0.21	0.73	0.0004388
Elusimicrobia	0.00	0.00	0.12	0.10	0.07	0.09	0.28	0.78	0.53	1.77	1.37	1.24	0.60	1.62	0.25	1.69	1.60	0.76	1.12	0.71	0.0006363
Deltaproteobacteria	13.52	5.76	3.53	2.63	3.38	3.27	3.57	2.02	1.20	1.61	0.86	0.39	0.42	0.75	0.64	0.93	0.56	1.30	0.43	-0.71	0.0007204
Planctomycetes	9.53	6.11	2.44	3.39	2.96	3.81	5.61	2.07	1.26	2.00	2.40	2.02	1.32	2.53	0.20	1.67	1.25	1.78	0.43	-0.73	0.0003605
Alphaproteobacteria	26.61	10.65	7.95	7.71	8.71	16.31	13.55	1.56	1.64	0.13	2.30	1.42	0.90	0.77	0.94	1.15	1.32	1.16	0.43	-0.75	0.0002193
WS3	0.64	0.87	0.17	0.42	0.23	0.34	0.20	0.18	0.12	0.16	0.17	0.18	0.00	0.14	0.00	0.08	0.07	0.08	0.00	-0.76	0.0001485
Spirochaetes	0.17	0.29	0.19	0.10	0.05	0.23	0.03	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.77	0.0001277

▲ Fig.4 Heat plot of bacterial phyla with significant change according to the depth of sediment core

- **Geochemistry within the core from surface to 100 cmbsf was distinguishable from that of sediments with other depth**
- **Candidate phyla were abundant in anoxic zone (20.0 - 63.1%) and especially OP8 and OP9 were dominant composing 22.3 to 58.1% of bacterial communities**
- ***Crenarchaeota* was the most abundant phyla (67.4 - 95.8%) throughout the core and *Thaumarchaeota*, which composed 66.7% at the surface decreased and Marine Benthic Group B (MBGB) increased from 3.2% upto 58.4% along depth at the class level of *Crenarchaeota***
- **High portion of eukaryotes (16.6 - 69.2%) was not assigned to any known eukaryotic groups and *Stramenopiles* (18.8 - 50.8%) was the most abundant throughout the core while *Alveolata* and *Metazoa* were abundant only in the subsurface of the sediment**
- **Vertical stratification of microbial communities in the core was remarkably distinguishable**

Conclusion

- **Drastic change of the microbial communities in oxic-anoxic transition zone was observed indicating microbial community structure can be directly correlated to geochemistry within these sediments**
- **The presence of candidate phyla or unassigned groups and their high proportion indicate their important ecological roles in deep-sea sediments and further studies to understand the roles or function of uncultured microbes in relation to geochemistry are necessary**

References

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