Macroscopic Biofilms in Fracture-Dominated Sediment that Anaerobically Oxidize Methane

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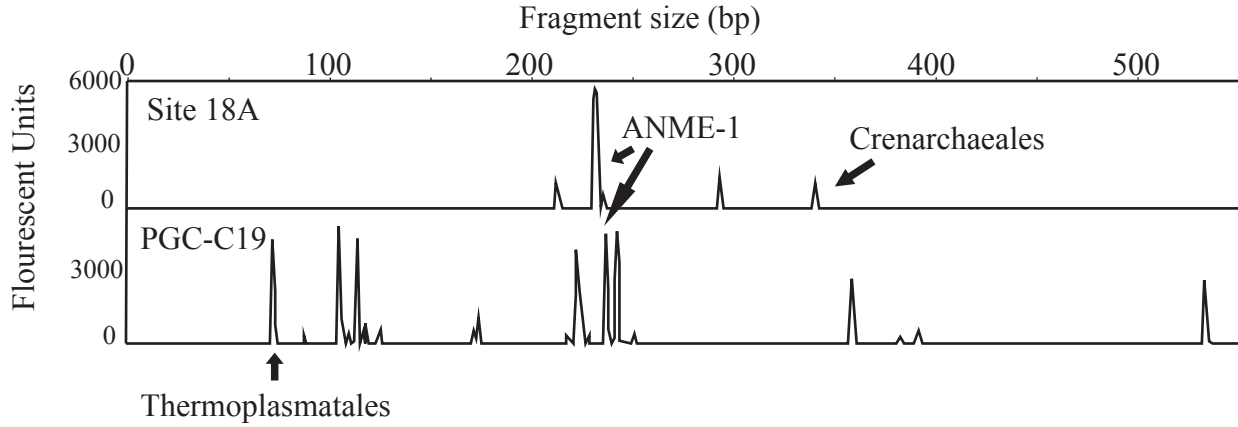Corvallis, OR 97331

Figure S1. Representative electropherograms obtained from archaeal terminal restriction fragment length polymorphism analysis from the biofilms at Site 18A (India) and PGC0807 (NCM). In silico digestion was performed on clone sequences and compared to peak sizes to determine the probable identity of archaeal peaks.

Figure S2. Neighbor-joining distance tree (created in FastTree (S1)) showing representative bacterial phylotypes derived from DNA extracted from subseafloor biofilms and then amplified (using 16S rRNA gene primers) and cloned. Representative biofilm phylotypes from this study are indicated in bold type. The solid circles at nodes indicate bootstrap values <40%. The designations in parentheses after the biofilm phylotypes indicate the number of clones obtained for a particular phylotype from either sediments from offshore India (I) or the northern Cascadia Margin (NCM).

slm_arc_800 (I:1)
Kidd Mud volcano, DGGE ANME−03 (EF484882)
marine sediment, TA1a9 (AF134387)
slm_arc_201 (I:1, NCM:29)
Aarhus Bay, Arch125 (FN428824)
slm_arc_400 (I:42)
phreatic sinkhole, Z273FA47 (FJ485500)
Kazan mud volcano, KZNMV−25−A3 (FJ712384)
slm_arc_110 (I:3)
Kazan mud volcano, KZNMV−30−A4 (FJ712394)

ANME-1

Methanomicrobiales

Kazan mud volcano, Kazan−2A−32/BC19−2A−32 (AY592008)
slm_arc_190 (I:2)
Coastal aquifer, 56S 3A 45 (DQ837291)

Cultured

ANME-2

ANME-3

Methanosarcinales

Cultured

Gulf of Mexico, GoM GC234 007R (AY211690)
slm_arc_130 (I:1)
South China Sea, MD2902−A2 (EU048591)
Hydrate Ridge, HydGC−84−92A (AM229261)
slm_arc_200 (I:1)
mangrove soil, MMS 203 (FJ477316)
slm_arc_180 (I:4)
hydrothermal vent, pMC2A203 (AB019737)
Hydrate Ridge, HydGC−84−240A (AM229257)
hypersaline microbial mat, C4 1G (EU570136)
slm_arc_160 (I:1)
Gulf of Mexico, SMI1−GC205−Arc48 (DQ521772)
cold seep, UT06 10 52A 59 (AB525478)
cold seep, UT06 10 52A 08 (AB525485)
slm_arc_150 (I:2)
AOM enrichment, AOM−Clone−F5 (FJ555680)
AOM bioreactor, AMOS1A 4113 D05 (AY323220)
slm_arc_140 (I:1, NCM:2)
marine sediment, TA1f2 (AF134390)
Gulf Mexico, SMI1−GC205−Arc38 (DQ521781)

Thermoplasmatales

Euryarchaeota

Crenarchaeota

slm_arc_900 (I:2)
Aarhus Bay, Arch101 (FN428820)
Hydrate Ridge, HR−CF−014 (DQ058814)
Hydrate Ridge, ODP204 30 ArchU62 (AM713455)
slm_arc_500 (I:1)
Haakon Mosby Mud Volcano, HMMVPog−30 (AJ579313)
Hydrate Ridge, Hyd24−Arch07b (AJ578114)

Crenarchaeales

Minami−Kanto Gas Field, MOB4−16 (DQ841222)
slm_arc_170 (I:1)
Juan de Fuca sediment, Mothra A6−1 (GQ267160)
slm_arc_100 (I:2)
South China Sea, BD72AR16 (GU363073)
slm_arc_700 (I:2)
marine sediment, MD3059S−16 (GQ927684)
slm_arc_210 (I:1)
Juan de Fuca sediment, Mothra A2−29 (GQ267172)
Mediterranean Sea, AMSMV−S1−A28 (FJ649522)
slm_arc_120 (I:1, NCM:1)
Aarhus Bay, Arch44 (FN428814)
slm_arc_220 (I:2, NCM:1)
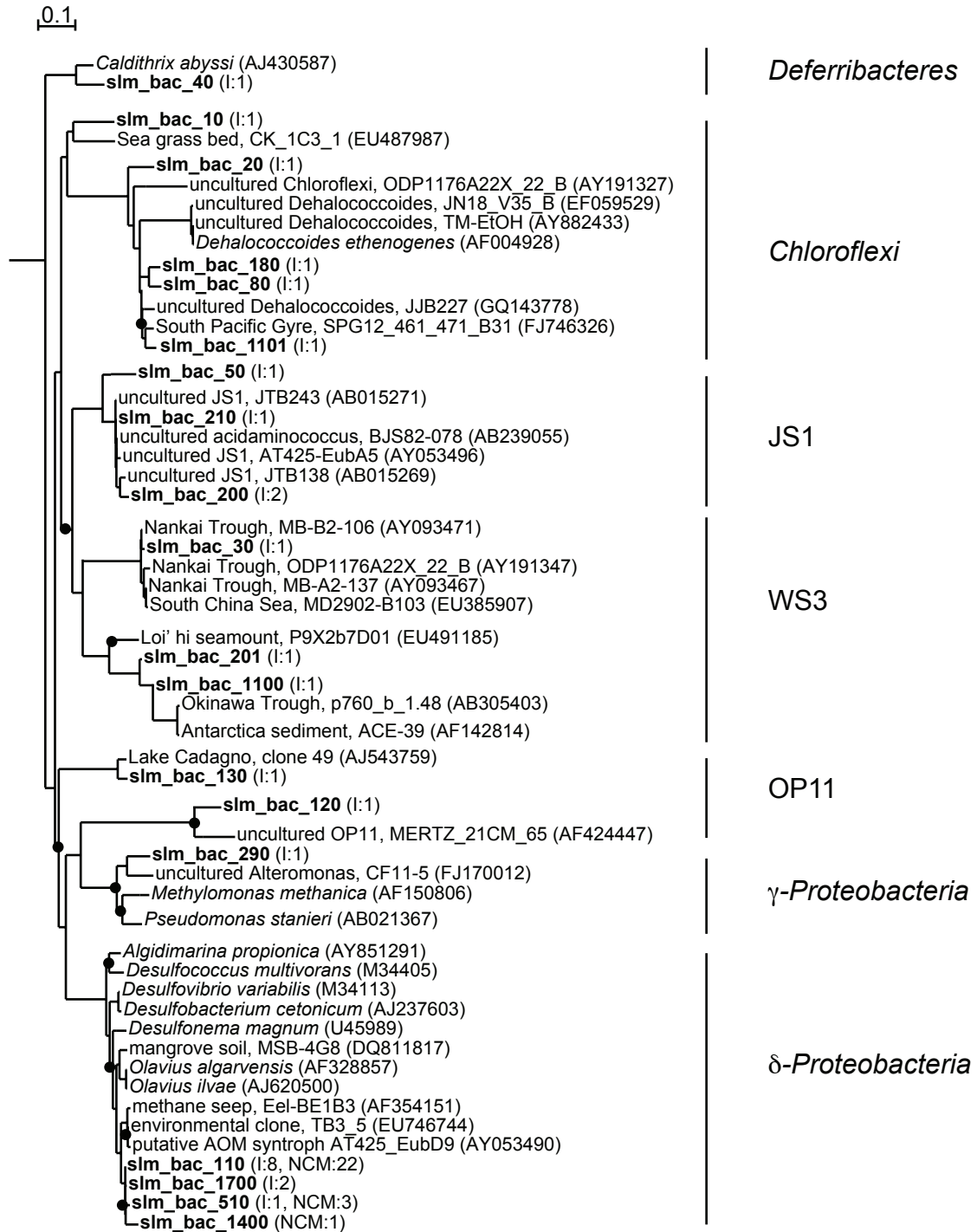Aarhus Bay, Arch43 (FN428813)

Desulfurococcales
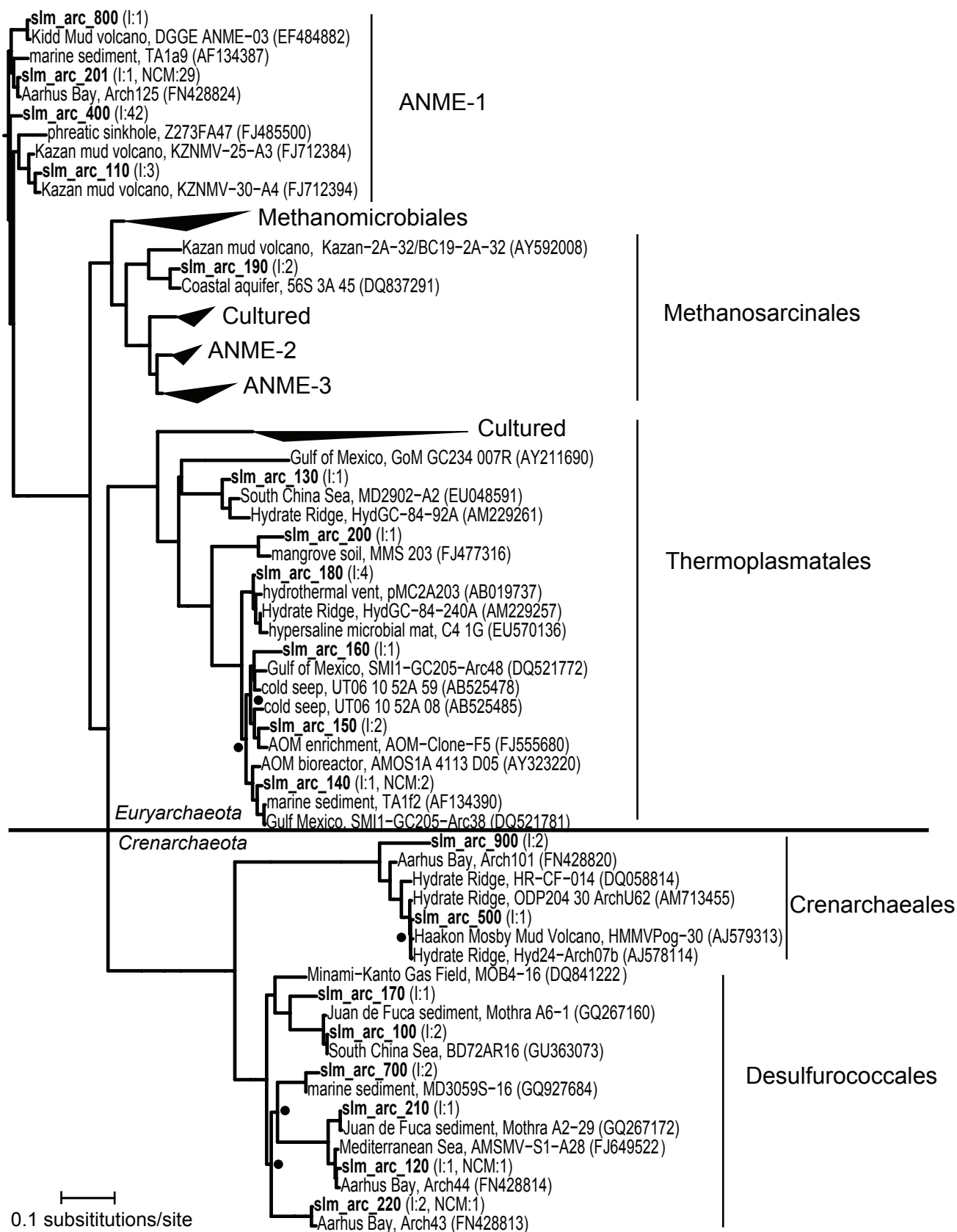
0.1 subsititutions/site

Figure S3. Neighbor-joining distance tree (created in FastTree (S1)) showing representative archaeal phylotypes derived from DNA extracted from subseafloor biofilms and then amplified (using 16S rRNA gene primers) and cloned. Representative biofilm phylotypes from this study are indicated in bold type. The solid circles at nodes indicate bootstrap values <40%. The designations in parentheses after the biofilm phylotypes indicate the number of clones obtained for a particular phylotype from either sediments from offshore India (I) or the northern Cascadia Margin (NCM).

Supplemental References

S1.   **Price, M. N., P. S. Dehal, and A. P. Arkin.** 2009. FastTree: computing large minimum evolution trees with profiles instead of a distance matrix. Mol. Biol. Evol. **26:**1641-50.