

Supplementary Material

Microbial diversity in a submarine hydrothermal chimney from the serpentinized system of the Prony Bay (New Caledonia) over a 6 years period.

Anne Postec^{1*}, Marianne Quéméneur¹, Méline Bes¹, Nan Mei¹, Fatma Benaïssa¹, Claude Payri², Bernard Pelletier², Christophe Monnin³, Linda Dombrowsky^{1,2}, Bernard Ollivier¹, Emmanuelle Gérard⁵, Céline Pisapia⁵, Martine Gérard⁴, Bénédicte Ménez⁵, Gaël Erauso^{1*}.

1 Aix Marseille Université, CNRS/INSU, IRD, Mediterranean Institute of Oceanography, UM110, 13288 Marseille, France

2 Institut pour la Recherche et le Développement, Centre de Nouméa, promenade Laroque, 98848 Nouméa, Nouvelle-Calédonie

3 Géosciences Environnement Toulouse, UMR 5563, 14 avenue Édouard Belin, 31400 Toulouse

4 Institut de Minéralogie et de Physique des Milieux Condensés, 4 place Jussieu, 75005 Paris, France

5 Institut de Physique du Globe de Paris, Sorbonne Paris Cité, Univ. Paris Diderot, CNRS, 75005 Paris, France

*** Correspondence: anne.postec@univ-amu.fr and gael.erauso@univ-amu.fr**

Supplementary Table 2. Primers used in this study for detection of 16S rRNA genes and functional genes (*dsrAB* and *mcrA* genes).

Primer	Sequence (5'→3')	Reference
Bacterial 16S rRNA genes		
27F	AGA GTT TGA TCM TGG CTC AG	(Lane, 1991)
907R	CCG TCA ATT CMT TTR AGT TT	(Lane, 1991)
341F*	CCT ACG GGA GGC AGC AG	(Muyzer et al., 1993)
518R	ATT ACC GCG GCT GCT GG	(Muyzer et al., 1993)
Archaeal 16S rRNA genes		
109F	ACK GCT CAG TAA CAC GT	(Webster et al., 2006)
958R	YCC GGC GTT GAM TCC AAT T	(Webster et al., 2006)
344F*	ACG GGG HGC AGC AGG CGC GA	(Raskin et al., 1994)
519R	GWA TTA CCG CGG CKG CTG	(Amann et al., 1995)
EURY498	CTT GCC CRG CCC TT	(Loy et al., 2003)
<i>mcrA</i> genes		
MLF	GGT GGT GTM GGA TTC ACA CAR TAY GCW ACA GC	(Luton et al., 2002)
MLR	TTC ATT GCR TAG TTW GGR TAG TT	(Luton et al., 2002)
ME2R'	TCA TBG CRT AGT TDG GRT AGT	(Nunoura et al., 2008)
ME3MF	ATG TCN GGT GGH GTM GGS TTY AC	(Nunoura et al., 2008)
ME3MF-e	ATG AGC GGT GGT GTC GGT TTC AC	(Nunoura et al., 2008)
<i>dsrAB</i> genes		
DSRp2060F	CAA CAT CGT YCA YAC CCA GGG	(Geets et al., 2006)
DSR4R	GTG TAG CAG TTA CCG CA	(Wagner et al., 1998)

* A 40-bp GC clamp was added to the 5' end for DGGE analysis: (5'-CGC CCG CCG CGC GCG GCG GGC GGG GCG GGG GCA CGG GGG G-3') (Sheffield et al., 1989).

References

- Amann, R.I., Ludwig, W., and Schleifer, K.-H. (1995). Phylogenetic identification and *in situ* detection of individual microbial cells without cultivation. *Microbiol. Rev.* 59, 143-169.
- Geets, J., Borremans, B., Diels, L., Springael, D., Vangronsveld, J., Van Der Lelie, D., and Vanbroekhoven, K. (2006). DsrB gene-based DGGE for community and diversity surveys of sulfate-reducing bacteria. *J. Microbiol. Meth.* 66, 194-205. doi: 10.1016/j.mimet.2005.11.002.
- Lane, D.J. (1991). "16S/23S rRNA sequencing,," in *Nucleic Acid Tech. Bact. Syst.*, ed. E.S.M. Goodfellow. (John Wiley and Sons, New York), 115-175.
- Loy, A., Horn, M., and Wagner, M. (2003). probeBase: an online resource for rRNA-targeted oligonucleotide probes. *Nucleic Acids Res.* 31, 514-516. doi: 10.1093/nar/gkg016.
- Luton, P.E., Wayne, J.M., Sharp, R.J., and Riley, P.W. (2002). The *mcrA* gene as an alternative to 16S rRNA in the phylogenetic analysis of methanogen populations in landfill. *Microbiology* 148, 3521-3530.
- Nunoura, T., Oida, H., Miyazaki, J., Miyashita, A., Imachi, H., and Takai, K. (2008). Quantification of *mcrA* by fluorescent PCR in methanogenic and methanotrophic microbial communities. *FEMS Microbiol. Ecol.* 64, 240-247.
- Raskin, L., Poulsen, L.K., Noguera, D.R., Rittmann, B.E., and Stahl, D.A. (1994). Quantification of methanogenic groups in anaerobic biological reactors by oligonucleotide probe hybridization. *Appl. Environ. Microbiol.* 60, 1241-1248.
- Sheffield, V.C., Cox, D.R., Lerman, L.S., and Myers, R.M. (1989). Attachment of a 40-base pair G+C-rich sequence (GC-clamp) to genomic DNA fragments by the polymerase chain reaction results in improved detection of single-base changes. *Proc. Natl. Acad. Sci. U.S.A.* 86, 232-236.
- Wagner, M., Roger, A.J., Flax, J.L., Brusseau, G.A., and Stahl, D.A. (1998). Phylogeny of dissimilatory sulfite reductases supports an early origin of sulfate respiration. *J. Bacteriol.* 180, 2975-2982.
- Webster, G., John Parkes, R., Cragg, B.A., Newberry, C.J., Weightman, A.J., and Fry, J.C. (2006). Prokaryotic community composition and biogeochemical processes in deep seafloor sediments from the Peru Margin. *FEMS Microbiol. Ecol.* 58, 65-85. doi: 10.1111/j.1574-6941.2006.00147.x.