Supplementary Material

Relative abundance and diversity of bacterial methanotrophs at the oxic-anoxic interface of the Congo deep-sea fan.

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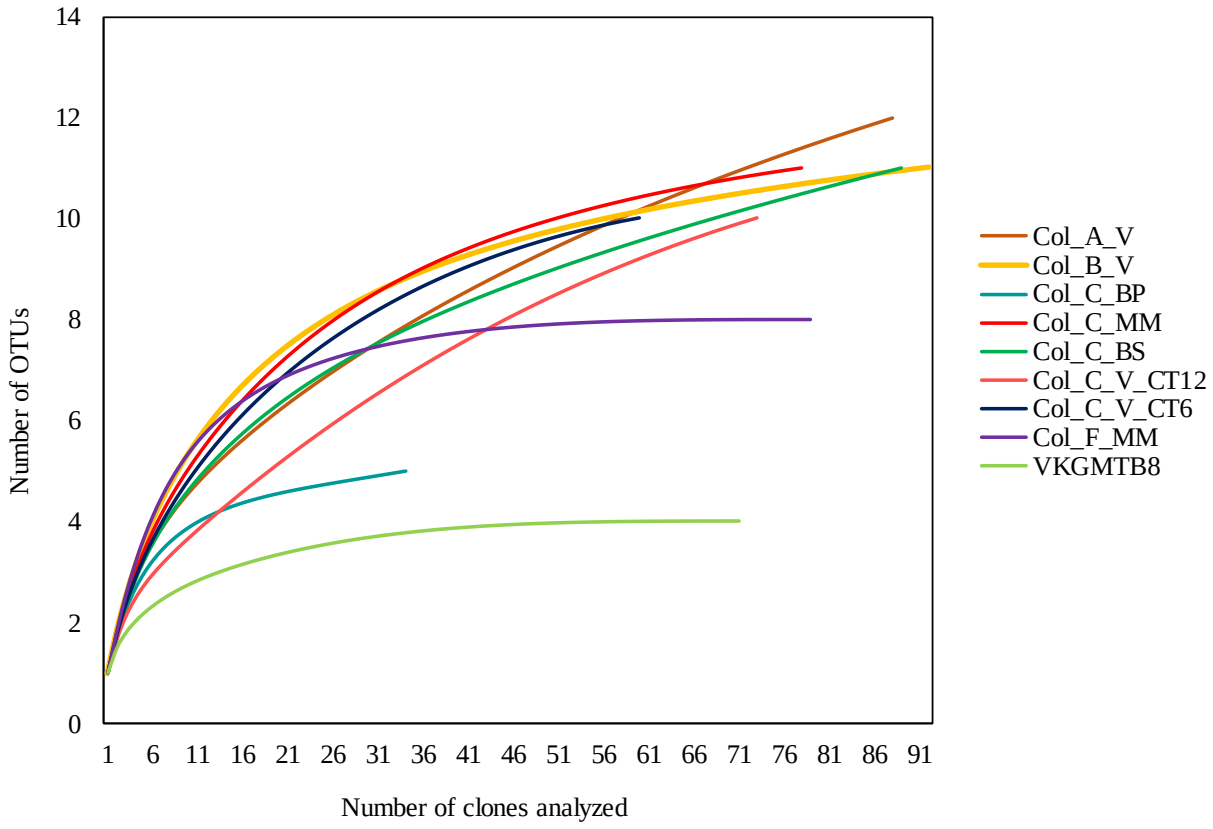
1 Supplementary Data

1.1 Geochemical analyses

Pore-water analyses were performed on replicate sediment push-cores using Rhizon samplers and methane (CH_4) concentrations were measured as described in (Vigneron et al., 2013). CH_4 fluxes at sediment-water interface were determined *in situ* by using a *Calmar* benthic incubation chamber (Caprais et al., 2010) deployed on almost every investigated habitats by the ROV Victor 6000 as described in (Khripounoff et al., 2015). Diffusive oxygen (O_2) uptake and oxygen penetration depth (OPD) in the bottom water and in the sediment were measured *in situ* and analyzed as described in (Rabouille et al., 2009).

2 Supplementary Figures and Tables

2.1 Supplementary Figures



Supplementary Figure 1: Rarefaction curves for *pmoA* sequences clustered at 93% similarity in surface organic-rich and seep sediments of habitats in the Congo deep-sea fan (Col) and Haakon Mosby volcano (VKGMTB8) respectively. Samples are grouped color wise based on location.

Supplementary Table 1: Methane (CH_4) concentration, CH_4 efflux, diffusive oxygen uptake (DOU) and oxygen penetration depth (OPD) at sediment-water interface of different organic-rich sedimentary habitats of the Congo deep-sea fan. [(a)] data from (Pastor et al., 2017), [(b)] data from (Khripounoff et al., 2016), [(c)] data from this study and [(d)] (Pozzato et al., Submitted). Abbreviations: PL: Dive number; CT: Push-cores number, Col: **Co**ngo **l**obe. V: Vesicomyids habitats; BP: Black patch sediment; BS: Brown sediment; MM: Microbial mat habitats. NA: Not assessed during the Congolobe cruise.

Sites	Sample name	*Ex situ* CH_4 concentration (µM) [a]	*In situ* CH_4 efflux (mmol m^{-2} d^{-1})	*In situ* DOU (mmol m^{-2} d^{-1}) [d]	*Ex situ* OPD (mm) [d]
site A	Col_A_V	3.2	108.5 [b]	20.5	0.8
site F	Col_F_MM	143.6	208.8	9.9	3.9
site C	Col_C_MM	5.3	NA	11.5	1.56
	Col_C_BP	124.7	94 c	20.7	1.3
	Col_C_V_CT6	7.1	NA	19.4	1.6
	Col_C_V_CT12	NA	NA	8.3	2.2
	Col_C_BS	0.2	2.4 [c]	2.6	11
site B	Col_B_V	<0.1	8.4 [b]	2.8	9.4
site E	Col_E_BS	<0.1	0.0 [c]	1.4	66.5

Supplementary Table 2: List of FISH probes used in this study.

Name	Target group	Sequence (5'- 3')	reference
Eub338-Alexa	Most of Bacteria	GCT-GCC-TCC-CGT-AGG-AGT	(Amann et al., 1990)
MTMC701-Cy3	*Methylococcales*	GTG TTC CTT CAG ATC TCT	(Boetius et al., 2000)
Mγ84-Cy3	Type I MOB	CCA-CTC-GTC-AGC-GCC-CGA	(Eller et al., 2001)
Mγ705-Cy3	Type I MOB	CTG-GTG-TTC-CTT-CAG-ATC	(Eller et al., 2001)
Mα450-Cy3	Type II MOB	ATC-CAG-GTA-CCG-TCA-TTA-TC	(Eller et al., 2001)

3 References

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