Supplementary information for

Adaptation of methane oxidising bacteria to environmental changes: implications for coastal methane dynamics

Authors

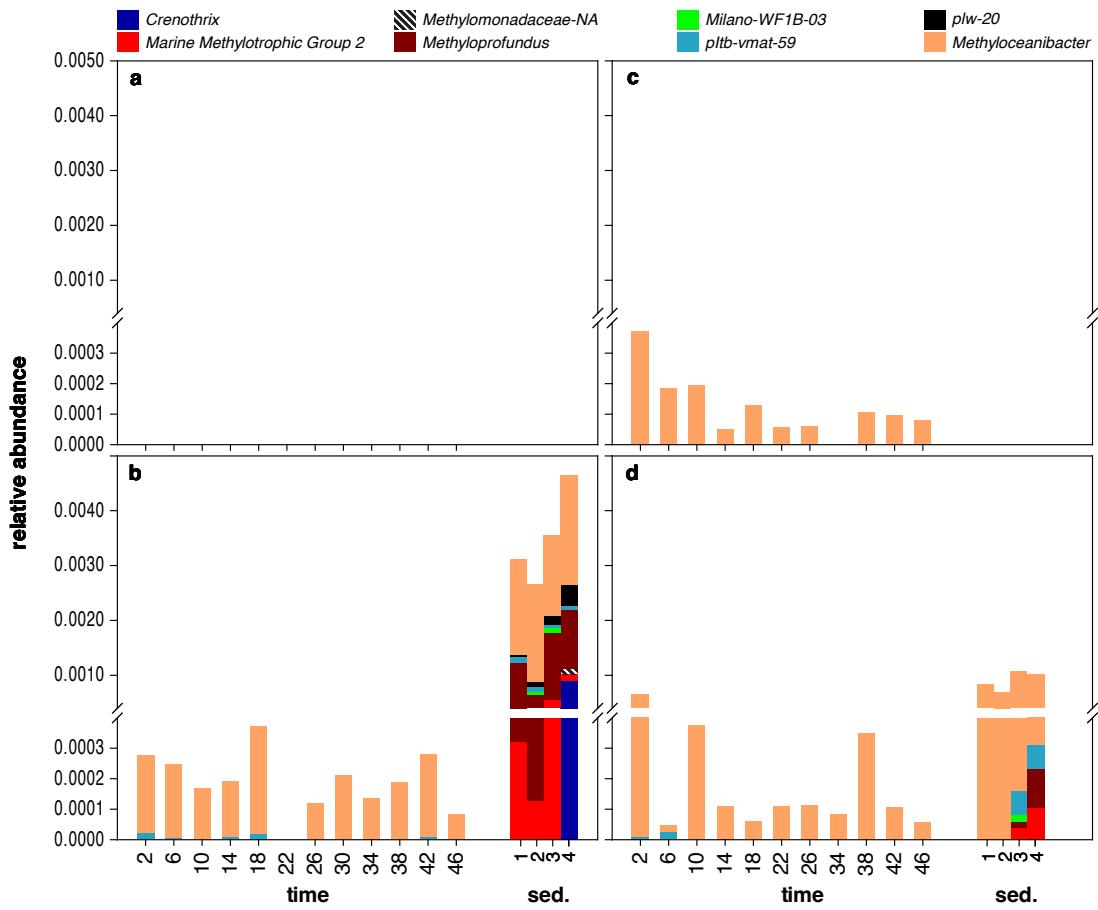
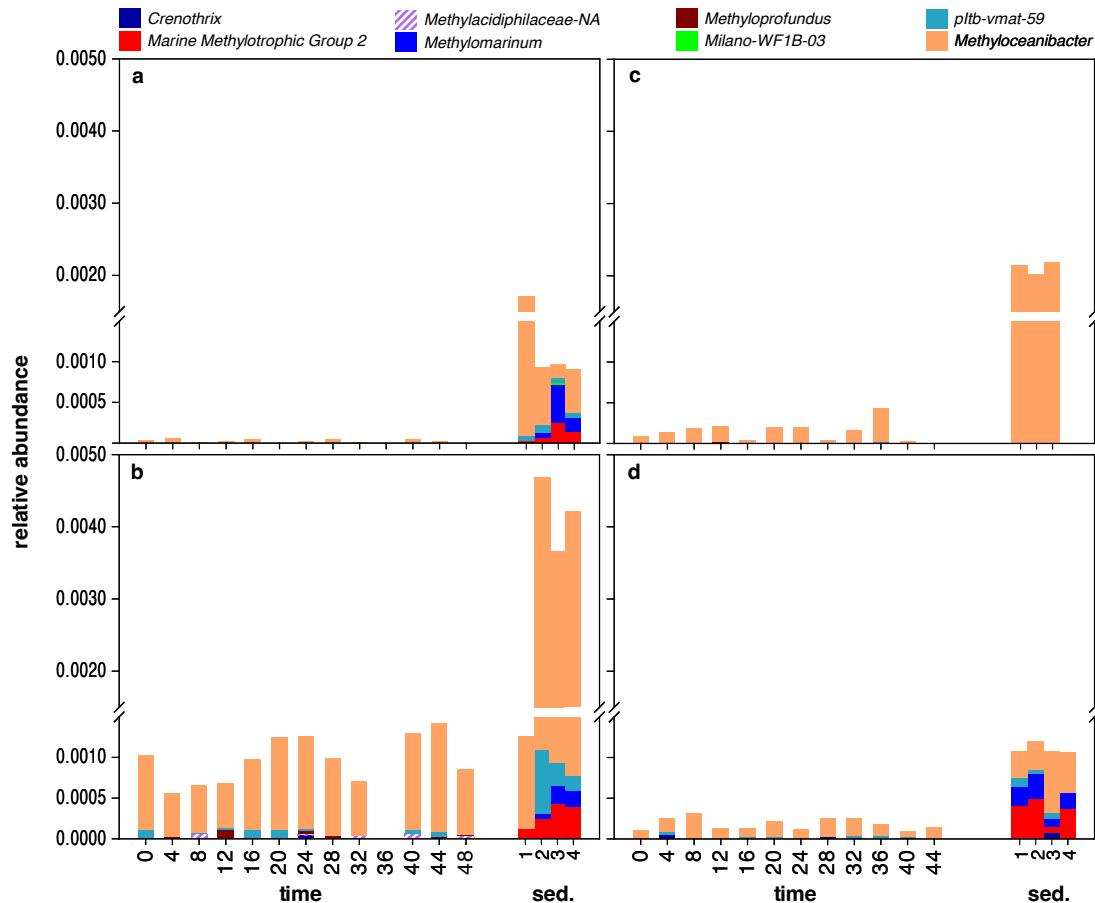
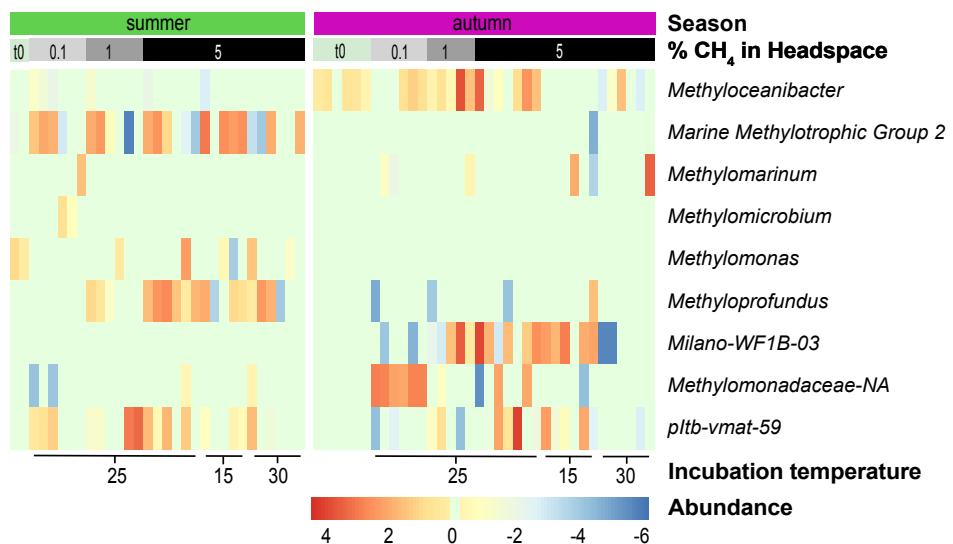
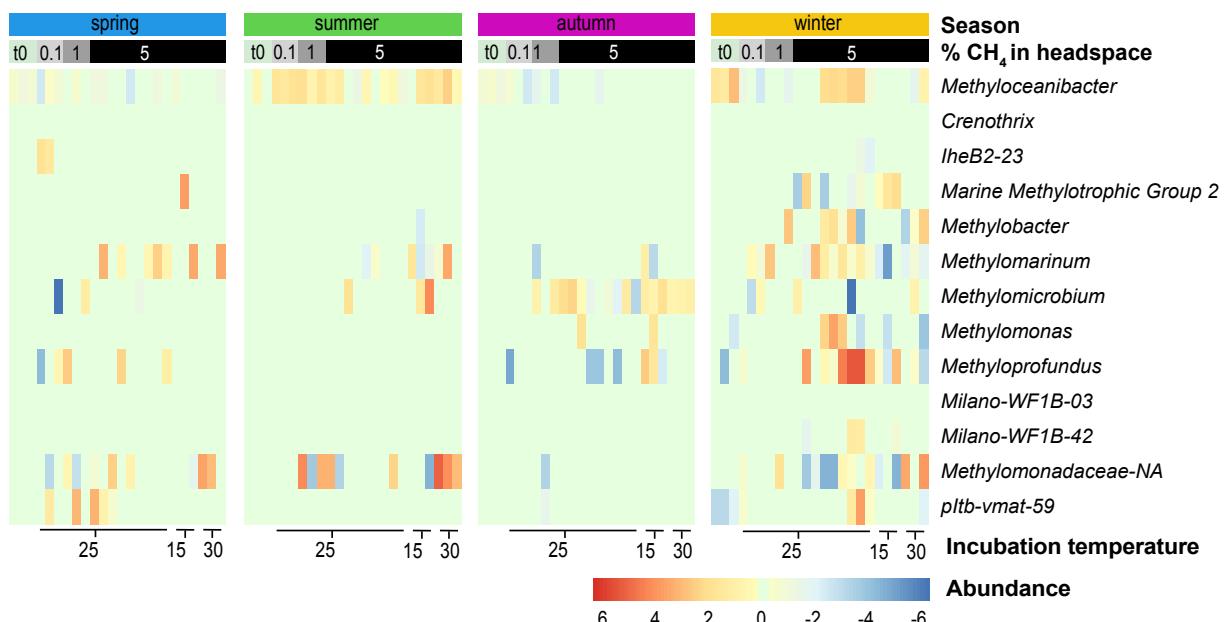
Tim R. de Groot[1], J.C. Engelmann[1*], P. Ramond[1,2], Julia Dorigo[1], Judith van Bleijswijk[1] and H. Niemann[1,3,4*]

1. NIOZ Royal Netherlands Institute for Sea Research, Texel, the Netherlands

2. Centro de Investigación Mariña (CIM), University of Vigo, Vigo, Spain

3. Department of Earth Sciences, Utrecht University, Utrecht, the Netherlands

4. CAGE – Centre of Arctic Gas Hydrate, Environment and Climate, Department of Geosciences, UiT the Arctic University of Norway, Tromsø, Norway

*corresponding authors:
julia.engelmann@nioz.nl
helge.niemann@nioz.nl

Supplementary Figure 1. Temporal and seasonal variation of environmental MOB communities in the North Sea water column and sediment. The x-axis indicates the time (in hours) during a repeated 48 h time-series of sampling during summer at depth of 10 m (a) and 35 m water depth (b) as well as during autumn at 10 m (c) and 35 m water depth (d). Surface sediments (sed.) sampled at the end of the time series during summer (b) and autumn (d) are indicated, too. MOB were below detection limit in summer at 10 m water depth; no sample are available for 35 m water depth at 22 and 34 hours in summer as well as at 10 m water depth at 34h hours in autumn. Note that not all MOBs found in the incubation experiments (Figure 1) could be detected in the initial water column or sediment samples.

Supplementary Figure 2. Temporal and seasonal variation of environmental MOB communities in the Wadden Sea water column and sediment. The x-axis indicates the time during a repeated 48 h time-series of sampling during spring (a), summer (b), autumn (c) and winter (d). Surface sediments (sed.) sampled at the end of the time series during summer (b) and autumn (d) are indicated, too. No samples are available for 36h hours in autumn and only three sediment samples are available for summer. Note that not all MOBs found in the incubation experiments (Figure 2) could be detected in the initial water column or sediment samples. Conversely, unidentified genera of the Methylacidiphilaceae potentially comprising MOB were not detected in the incubation experiments.

Supplementary Figure 3. Heatmap of MOB abundances (centered log-ratio transformed counts) observed in North Sea (a) and Wadden Sea incubations (b), categorised by season and headspace methane concentration. Red color indicates higher abundance, blue indicates lower abundance of a particular MOB genus compared to the geometric mean of the respective sample.

1 **Supplementary Table 1**. Phylogeny of known aerobic methane oxidising bacteria (note that
2 Candidatus Mehtylomirabilis utilises nitrate/nitrite for methane oxidation; Ettwig et al.,). See
3 also Dedysh and Knief (2018), and Haque et al. (2020).

Type	Phylum	Order	Family	Genus
I	Gammaprteobacteria	Methylococcales	Methylomonadaceae	Crenothrix
				ET-SHO
				IheB2-23
				Incertae Sedis
				Marine Methylotrophic Group 2
				Methylicorpusculum
				Methylobacter
				Methyloglobulus
				Methylomarinum
				Methylomicrobium
				Methylomonas
				Methyloprofundus
				Methylosarcina
				Methylosoma
				Methylosphaera
				Methylotuvimicrobium
				Methylovulum
				Milano-WF1B-03
				Milano-WF1B-42
				pItb-vmat-59
				pLW-20
			Methylococcacea	Candidatus Methylospira
				Incertae Sedis
				Methylocaldum
				Methylococcus
				Methylogaea
				Methylomagnum
				Methyloparacoccus
				Methyloterricola
			Methylohalobiaceae	Methylohalobius
				Methylomarinovum
				Methylothermus
II	Alphaproteobacteria	Hyphomicrobiales	Beijerinckiaceae	Methylosinus
				Methylocystis
				Methylocella
				Methylocapsa
				Methyloferula
			Methyloligellaceae	Methyloceanibacter
III	Verrucomicrobiota	Methylacidiphilales	Methylacidiphilaceae	Methylacidiphilum
				Methylacidimicrobium
	Methylomirabilota	Methylomirabilales	Methylomirabilaceae	Candidatus Mehtylomirabilis

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1   Supplementary files available at DAS (provisional DOI Nr: 10.25850/nioz/7b.b.6h)

2   - configuration file of the Cascabel pipeline (Suppl_Information_1_config_Cascabel.yaml)

3   - ASV table (asv_table.csv)

4   - Taxonomy assignment of ASVs (taxotable.csv)

5   - sample metadata (filtered_metadata.csv)

6   - R-script for filtering out MOB and relative abundance calculation (asv_mob_RA.R)

7   - R-script for DESeq of North Sea samples (DESeq_NS.R)

8   - R-script for DESeq of Wadden Sea samples (DESeq_WS.R)

9   - R-script for NMDS of whole community (nmds_whole community.R)

10   - R-script for NMDS of MOB (nmds_MOB.R)

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12   *The data archive can be accessed at https://dataverse.nioz.nl (username = 7b.b.6h, PW =*
13   *e342ad68).*
14   *How to access the page:*
15   *- go to https://dataverse.nioz.nl*
16   *- Select 'Log In' from the upper menu bar*
17   *- Enter the credentials provided above and click the 'Login'-button below*
18   *- Click the name of the data owner (Helge Niemann) from the top menu bar and select 'My*
19   *Data' from the menu. This will exclusively display the landing page of interest.*
20   *- Click on the title of the data set (Adaptation of methane oxidising bacteria to environmental*
21   *changes: implications for coastal methane dynamics - data and scripts). This will display a*
22   *list of downloadable files*
23
24   *Upon acceptance, a final DOI number and publicly open database will be made available*

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