



SUPPLEMENTARY MATERIALS FOR

Methanogenic Biodegradation of *iso*-Alkanes by Indigenous Microbes from Two Different Oil Sands Tailings Ponds

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The supplementary materials contain 1 figure (Figure S1) and 2 tables (Table S1 and S2).

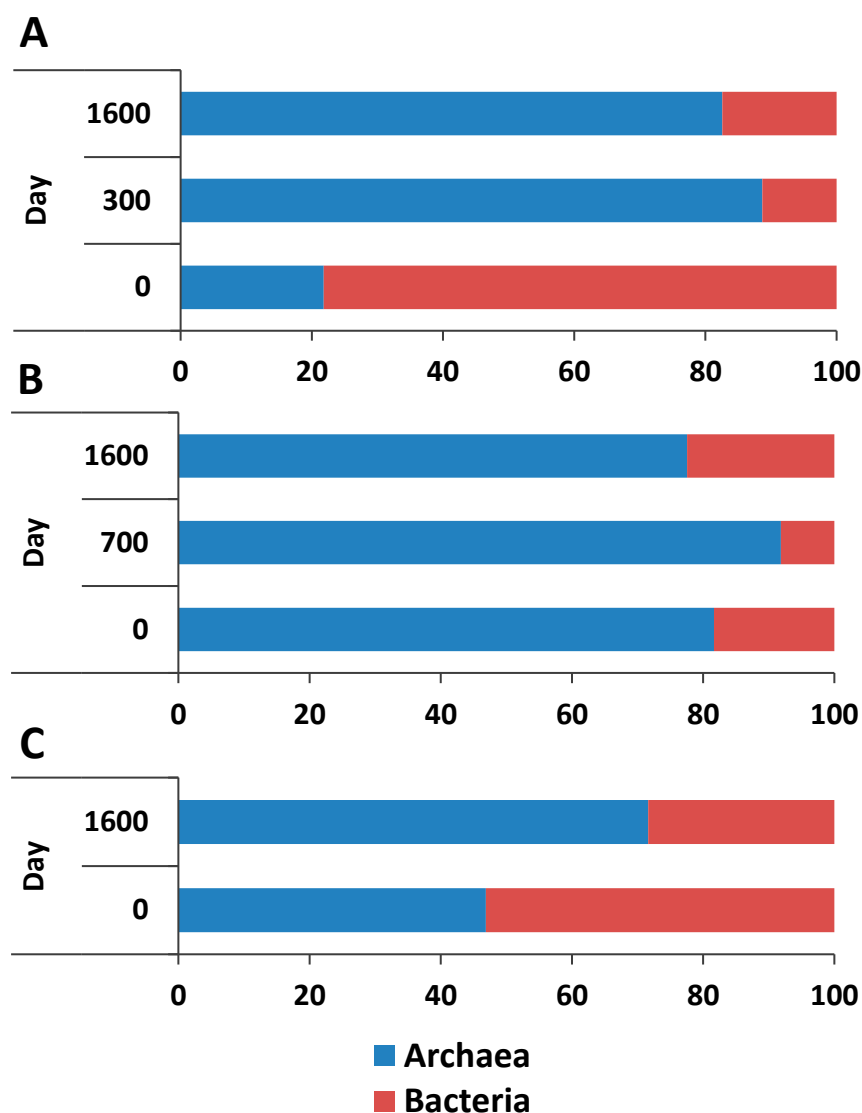


Figure S1. Archaeal and bacterial reads expressed as a proportion of total quality-controlled prokaryotic reads, based on analysis of partial 16S rRNA gene pyrosequences before and during incubation of MFT with *iso*-alkanes mixtures. **(A)** CNUL MFT amended with M-3I; **(B)** CNRL MFT amended with M-3I; and **(C)** CNRL MFT amended with M-5I. The results represent pooled amplicons of triplicate cultures.

Table S1. Relative abundance of bacterial 16S rRNA gene pyrosequences, grouped at class level, in CNUL and CNRL MFT incubated with mixtures of either three or five *iso*-alkanes (M-3I or M-5I) under methanogenic conditions. Analyses were performed on MFT before degradation (day 0) and after incubation times indicated in days. Genus assignments are shown where confident. “Others <5%” is the sum of all taxa individually abundant at <5% of the total bacterial reads in a given sample.

Nomenclature	CNUL			CNRL				
	M-3I			M-3I			M-5I	
				Day				
	0	300	1600	0	700	1600	0	1600
Actinobacteria								
<i>Coriobacteriales</i> ; <i>Coriobacterineae</i> ; <i>Coriobacteriaceae</i>	0.1	1.0	1.0	11.3	1.4	1.7	4.9	0.2
Anaerolineae								
<i>Anaerolineales</i> ; <i>Anaerolineaceae</i> ; <i>Leptolinea</i>	0.6	5.1	3.5	3.6	2.8	1.2	7.2	1.6
<i>Anaerolineales</i> ; <i>Anaerolineaceae</i> ; uncultured	0.4	7.2	12.2	10.3	2.8	4.0	13.8	2.7
Clostridia								
<i>Clostridiales</i> ; Family XI Incertae Sedis	0.0	0.0	6.2	0.4	0.7	2.9	0.3	0.1
<i>Clostridiales</i> ; <i>Peptococcaceae</i>	0.2	60.8	14.1	3.6	76.6	21.0	2.6	0.0
Betaproteobacteria								
<i>Burkholderiales</i> ; <i>Comamonadaceae</i>	0.1	0.0	1.8	0.2	0.0	4.7	8.9	0.3
<i>Hydrogenophilales</i> ; <i>Hydrogenophilaceae</i> ; <i>Thiobacillus</i>	93.8	0.0	1.3	0.3	0.7	1.8	0.1	0.0
<i>Rhodocyclales</i> ; <i>Rhodocyclaceae</i>								
<i>Rhodocyclales</i> ; <i>Rhodocyclaceae</i> ; uncultured	0.0	0.0	2.3	8.9	0.0	4.0	4.5	0.1
Deltaproteobacteria								
<i>Syntrophobacteriales</i> ; <i>Syntrophaceae</i> ; <i>Smithella</i>	0.0	1.0	0.5	9.7	1.4	1.8	8.5	86.1
Gammaproteobacteria								
<i>Pseudomonadales</i> ; <i>Pseudomonadaceae</i> ; <i>Pseudomonas</i>	0.6	0.0	12.9	0.1	0.0	5.6	0.2	0.1
Spirochaetes								
<i>Spirochaetales</i> ; <i>Spirochaetaceae</i> ; uncultured	0.0	2.1	1.0	3.4	0.0	1.3	8.0	0.4
Others (<5%)	4.1	22.7	43.3	48.2	13.5	50.1	40.9	8.3

Table S2. Relative abundance of archaeal 16S rRNA gene pyrosequences, grouped at class level, in CNUL and CNRL MFT incubated with mixtures of either three or five *iso*-alkanes (M-3I or M-5I) under methanogenic conditions. Analyses were performed on MFT before degradation (day 0) and after incubation times indicated. Genus assignments are shown where confident. “Others <5%” is the sum of all taxa individually abundant at <5% of the total archaeal reads in a given sample.

Nomenclature	CNUL			CNRL				
	M-3I			M-3I			M-5I	
				Day				
	0	300	1600	0	700	1600	0	1600
Methanobacteriales								
<i>Methanobacteriaceae</i> ; <i>Methanobacterium</i>	8.5	0.0	0.4	0.4	0.0	29.7	0.6	0.2
Methanomicrobiales								
<i>Methanoregula</i>	3.9	17.6	31.7	61.5	86.1	37.3	84.5	21.0
<i>Methanolinea</i>	8.9	37.6	0.6	0.0	0.1	0.0	0.0	0.0
Methanosarcinales								
<i>Methanosaetaceae</i> ; <i>Methanosaeta</i>	64.1	43.9	27.7	33.3	10.5	4.0	6.9	75.2
<i>Methanosarcinaceae</i> ; <i>Methanosarcina</i>	11.2	0.4	35.4	0.3	0.3	26.3	0.2	0.0
Others (<5%)	3.3	0.4	4.2	4.4	3.0	2.7	7.9	3.6