

Temporal microbial community dynamics in microbial electrolysis cells – influence of acetate and propionate concentration

Ananda Rao Hari ^{a*}, Krishnaveni Venkidusamy ^b, Krishna Katuri^a, Samik Bagchi^c, and Pascal E. Saikaly^{a*}

^aKing Abdullah University of Science and Technology, Biological and Environmental Sciences and Engineering Division, Water Desalination and Reuse Research Center, Thuwal 23955-6900, Saudi Arabia

^bCentre for Environmental Risk Assessment and Remediation (CERAR), University of South Australia, Mawson Lakes, South Australia, Australia

^cUniversity of Kansas, Department of Civil, Environmental, and Architectural Engineering, Lawrence, KS, USA 66045

*** Correspondence:**

Corresponding Authors Dr. Ananda Rao Hari (hari.anandarao@kaust.edu.sa) and Prof. Pascal Saikaly (pascal.saikaly@kaust.edu.sa)

Supporting Information

Table S1. The relative abundance of bacterial phylotypes classified to the lowest level possible (class, order, family or genus) for A-reactors: A, anode. Bacterial phyla representing less than 1% of the relative abundance presented as others in the table. The numbers after the symbols represent the sampling periods.

Taxa level (class)	Taxa level (order, family or genus)	A(AL-0)	A(AL-10)	A(AL-30)	A(AL-50)	A(AL-70)	A(AH-0)	A(AH-15)	A(AH-35)	A(AH-70)
<i>Deltaproteobacteria</i>	<i>Geobacter</i>	0.5±0.3	50.37±4.2	66.52±3.7	55.46±3.5	35.56±4	0.8±0.4	52.73±2.1	47.27±3.6	45.7±4.3
	<i>Desulfovibrio</i>	0.2±0.1	2.59±1.6	1.38±0.43	3.46±2.5	9.35±3.8	0.5±0.3	1.70±1	3.58±2.1	4.77±2.7
	<i>Desulfuromonadales</i>	4.51±1.9	0.5±0.3	0.00	0.00	0.00	1.09±0.7	0.5±0.4	0.3±0.2	0.00
	<i>Pelobacteraceae</i>	0.00	1.18±0.7	1.81±0.5	4.19±2.3	4.62±2.2	23.28±7.4	4.14±1.9	1.17±0.6	0.7±0.5
<i>Clostridia</i>	<i>Coprothermobacter</i>	57.83±8.7	20.71±5.6	11.39±4.9	8.53±4.3	8.56±4.8	33.98±5.5	9.84±3.7	14.31±5.4	11.07±3.3
	<i>Sedimentibacter</i>	0.00	0.00	0.00	0.00	0.00	0.6±0.4	1.74±0.8	2.03±1	0.7±0.5
	<i>Soehngenia</i>	1.68±0.9	2.81±2.2	0.5±0.3	2±1.1	1±0.6	5.53±2.5	3.58±2.7	4.3±2.3	2.58±2.5
	<i>Clostridiaceae</i>	0.00	0.00	0.5±0.4	0.7±0.4	0.7±0.6	0.00	0.3±0.2	0.4±0.3	0.3±0.1
<i>Synergistia</i>	<i>Dethiosulfovibrionaceae</i>	4.48±2.6	5.70±2.9	3.15±2.1	3.90±2	3.60±1.8	4.34±2.2	1.70±1	1.32±0.7	0.7±0.4
	<i>Synergistaceae</i>	4.33±2.3	1.02±0.5	1.56±0.8	0.7±0.6	1.52±0.7	1.90±1.1	0.7±0.5	0.5±0.3	0.8±0.5
<i>Betaproteobacteria</i>	<i>Rhodocyclaceae</i>	0.00	0.00	0.00	0.3±0.2	0.2±0.1	1.36±0.7	0.7±0.5	1.82±0.9	0.5±0.3
	<i>Thauera</i>	0.00	0.00	0.2±0.2	0.4±0.3	0.2±0.1	0.00	0.3±0.3	0.6±0.4	0.5±0.5
<i>Gammaproteobacteria</i>	<i>Pseudomonadaceae</i>	0.3±0.1	0.5±0.4	0.3±0.1	3±1.7	3.3±2.1	2.13±1.2	1.47±0.8	1.6±1	0.5±0.3
	<i>Pseudomonas</i>	0.2±0.2	0.30	0.70	2.10	8.60	0.30	0.20	1.30	4.00
	<i>Shewanella</i>	0.00	0.00	0.00	0.5±0.5	0.8±0.5	0.00	1.47±0.8	1.59±0.7	0.3±0.2
<i>Anaerolineae</i>	<i>Anaerolinaceae</i>	4.04±1.9	2.29±1.7	0.5±0.4	0.3±0.1	0.00	0.00	0.5±0.4	1.35±0.7	9.90±4.3
<i>Bacteroidia</i>	<i>Bacteroidales</i>	0.3±0.2	0.2±0.1	0.00	0.00	0.00	2.06±1.5	0.7±0.5	1.91±1	0.5±0.3
	<i>Porphyromonadaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.6±0.4	1±0.6	3±1.8
Others		21.6±5.1	11.29±3.4	11.46±4.1	14.44±3.8	21.95±3.6	22.09±4.3	17.08±2.6	13.57±4.5	13.43±3.3

Supporting Information

Table S2. The relative abundance of bacterial phylotypes classified to the lowest level possible (class, order, family or genus) for A-reactors: S, suspension. Bacterial phyla representing less than 1% of the relative abundance presented as others in the table. The numbers after the symbols represent the sampling periods.

Taxa level (class)	Taxa level (order, family or genus)	S(AL-0)	S(AL-10)	S(AL-30)	S(AL-50)	S(AL-70)	S(AH-0)	S(AH-15)	S(AH-35)	S(AH-70)
<i>Deltaproteobacteria</i>	<i>Geobacter</i>	0.00	18.59±3.7	28.72±2.2	29.72±2.9	14.12±3.3	0.00	30.37±1.9	9.97±5.7	45.31±3.1
	<i>Desulfovibrio</i>	0.00	1.21±0.7	3.09±1.2	14.41±2.8	6.91±3.1	0.00	2.17±0.9	4.87±2.2	5.53±3.2
	<i>Pelobacteraceae</i>	0.00	0.3±0.1	1.60±0.5	2.23±1	0.6±0.4	1.41±0.6	1.47±0.8	0.3±0.3	0.2±0.1
<i>Clostridia</i>	<i>Coprothermobacter</i>	47.11±6.3	31.38±4.9	3.17±1.4	3.40±1	0.4±0.2	39.15±4.6	4.17±1.7	11.67±2.9	1.08±0.5
	<i>Sedimentibacter</i>	0.3±0.2	0.7±0.4	4.90±1.8	1.83±0.7	0.6±0.4	0.4±0.4	7.32±3.3	5.09±2.3	0.7±0.4
	<i>Soehngenia</i>	2.95±1.8	2.13±1.1	0.4±0.3	0.2±0.2	0.00	12.31±3.6	1.52±0.8	0.4±0.3	0.3±0.3
	<i>Desulfosporomusa</i>	0.4±0.3	0.7±0.5	5.81±2.6	2.63±1.9	8.07±3.1	0.2±0.1	1.04±0.5	6.29±2.9	1.76±0.8
	<i>Clostridiaceae</i>	1.17±0.5	0.7±0.4	0.4±0.4	0.2±0.1	0.3±0.3	0.00	0.8±0.6	2.81±1.5	0.5±0.4
	<i>Oscillospira</i>	0.00	0.00	0.00	0.2±0.2	0.3±0.1	0.00	0.5±0.3	0.3±0.3	0.00
<i>Synergistia</i>	<i>Dethiosulfovibrionaceae</i>	5.16±3	2.86±2.1	0.6±0.5	8.53±2.5	1.99±1.1	7.37±3.4	0.5±0.5	1.84±0.7	0.7±0.4
	<i>Synergistaceae</i>	6.92±3.6	1.99±0.9	0.5±0.3	1.13±0.7	0.7±0.5	5.76±2.2	5.8±3.5	0.8±0.6	7±3.6
<i>Betaproteobacteria</i>	<i>Betaproteobacteria</i>	1±0.6	8±3.9	7.20±3.7	3.13±1.3	1.35±0.7	0.3±0.2	1.00±0.6	3.68±1.4	0.5±0.3
	<i>Dechloromonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.6±0.5	0.7±0.6	6.37±3.8
	<i>Rhodocyclaceae</i>	0.00	0.00	0.00	0.00	0.00	0.5±0.4	2.61±1.1	18.66±5.3	2.08±0.9
	<i>Alcaligenaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.4±0.2	0.3±0.2
<i>Gammaproteobacteria</i>	<i>Pseudomonadaceae</i>	0.7±0.7	5.2±2.7	16.5±4.3	1.1±0.6	31.3±4.2	4.83±2.2	16.1±4.1	0.9±0.6	14±4.7
	<i>Pseudomonas</i>	0.4±0.4	4.2±2.4	3.1±1.6	2±1.1	7.8±3.3	0.3±0.2	3.3±1.5	0.5±0.4	0.3±0.3
	<i>Shewanella</i>	0.00	0.3±0.3	6.38±3.3	0.4±0.3	0.4±0.4	0.00	4.97±2.6	0.8±0.6	4.00±2.2
<i>Anaerolineae</i>	<i>Anaerolinaceae</i>	1.97±0.9	1.23±0.7	0.2±0.1	0.00	0.00	1.37±0.8	0.4±0.3	2.42±1.4	2.07±1
<i>Bacteroidia</i>	<i>Bacteroidales</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.4±0.3	0.3±0.2
	<i>Porphyromonadaceae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.7±0.6	2.6±1.5	0.5±0.5
	<i>Parabacteroides</i>	0.00	0.00	1.41±0.8	0.5±0.4	0.3±0.3	0.00	0.6±0.5	4±2.1	0.4±0.3
	<i>Dysgonomonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.3±0.2	0.6±0.6
<i>Actinobacteria</i>	<i>Leucobacter</i>	3.82±2.2	3.06±1.7	0.5±0.5	0.00	0.00	0.00	0.00	0.00	0.00
Others		30±5.7	20.88±4.5	17.09±4	30.91±6.1	27.72±5.3	27.77±6.4	18.21±5.8	26.04±5.5	16.01±4.7

Supporting Information

Table S3. The relative abundance of bacterial phylotypes classified to the lowest level possible (class, order, family or genus) for P-reactors: A, anode. Bacterial phyla representing less than 1% of the relative abundance presented as others in the table. The numbers after the symbols represent the sampling periods.

Taxa level (class)	Taxa level (order, family or genus)	A (PL-0)	A (PL-10)	A (PL-30)	A (PL-50)	A (PL-70)	A (PH-0)	A (PH-20)	A (PH-35)	A (PH-70)
<i>Deltaproteobacteria</i>	<i>Geobacter</i>	1.38±0.5	72.71±5.1	70.73±7.8	66.14±5.5	38.78±2.3	11.52±1.8	48.74±6.1	23.25±2.7	41.86±6.2
	<i>Desulfovibrio</i>	0.6±0.4	1.83±0.8	3.43±1.5	11.39±3.2	9.22±3.8	0.0	1.58±1	0.4±0.2	1.20±0.4
	<i>Desulfuromonadales</i>	2.58±0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	<i>Pelobacteraceae</i>	10.76±3.2	0.0	0.0	0.0	0.0	2.32±0.8	0.0	0.0	0.0
	<i>Syntrophobacter</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3±0.2	0.3±0.1
<i>Clostridia</i>	<i>Coprothermobacter</i>	24.87±7.4	2.79±1.2	2.79±1.2	1.98±0.7	2.30±1.1	19.83±4.2	12.78±2.9	5.27±2.3	1.41±1
	<i>Sedimentibacter</i>	2.46±1.1	0.0	1.28±0.5	0.4±0.3	1.15±0.6	0.5±0.3	5.67±2.4	2.54±1.1	1.61±0.9
	<i>Syntrophomonas</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.5±0.4	1.99±0.9	0.5±0.3
	<i>Soehngenia</i>	3.74±1.7	0.96±0.3	1.32±0.5	0.0	0.0	1.46±0.6	1.33±0.4	0.4±0.1	0.3±0.1
	<i>Clostridiales</i>	0.4±0.4	0.0	0.0	0.0	0.0	0.3±0.3	0.6±0.2	3.46±1.5	5±1.8
<i>Synergistia</i>	<i>Dethiosulfovibrionaceae</i>	6.61±2.8	6.10±2.7	5.04±2.1	5.77±1.5	9.64±2.7	7.72±2.5	3.31±0.8	22.82±5.3	2.86±1.5
	<i>Synergistaceae</i>	4.93±2.1	0.67±0.2	0.0	0.2±0.3	5.2±1.8	7.19±1.8	0.5±0.2	4.1±1.7	1.53±0.8
<i>Betaproteobacteria</i>	<i>Dechloromonas</i>	1.3±0.9	0.0	2.19±0.9	0.5±0.2	0.4±0.2	2.97±1.5	2.25±1.2	0.7±0.5	0.6±0.2
	<i>Rhodocyclaceae</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	<i>Thauera</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3±0.1	4.52±2.4
<i>Gammaproteobacteria</i>	<i>Pseudomonadaceae</i>	0.93±0.3	0.2±0.1	0.3±0.3	0.3±0.2	1.25±0.7	1.56±0.4	0.4±0.2	0.4±0.2	3.8±1.1
	<i>Shewanella</i>	0.0	0.0	0.0	0.0	0.0	0.7±0.3	5.42±1.8	0.5±0.2	5.73±2.3
<i>Anaerolineae</i>	<i>Anaerolinaceae</i>	15.44±3.9	5.19±2.1	5.15±2.3	5.17±2.3	14.98±3.2	15.55±3.6	6.02±2.4	13.69±3.7	4.98±1.9
<i>Bacteroidia</i>	<i>Porphyromonadaceae</i>	2.38±1.1	0.0	0.0	1.76±0.7	1.25±0.8	1.58±0.9	0.4±0.3	1.17±0.8	1.49±0.5
	<i>Bacteroidales</i>	0.3±0.3	0.0	0.0	0.0	0.0	1.30±0.7	0.3±0.1	0.2±0.1	0.4±0.2
<i>Actinobacteria</i>	<i>Leucobacter</i>	2.62±1.2	0.0	0.0	0.0	0.0	2.13±0.9	0.6±0.3	1.07±0.6	1.2±0.8
Others		18.7±3.5	9.5±2.8	7.7±2.8	6.4±2.3	15.8±2.5	23.3±5.2	9.6±3.7	17.4±4.1	20.7±4.5

Supporting Information

Table S4. The relative abundance of bacterial phylotypes classified to the lowest level possible (class, order, family or genus) for P-reactors: S, suspension. Bacterial phyla representing less than 1% of the relative abundance presented as others in the table. The numbers after the symbols represent the sampling periods.

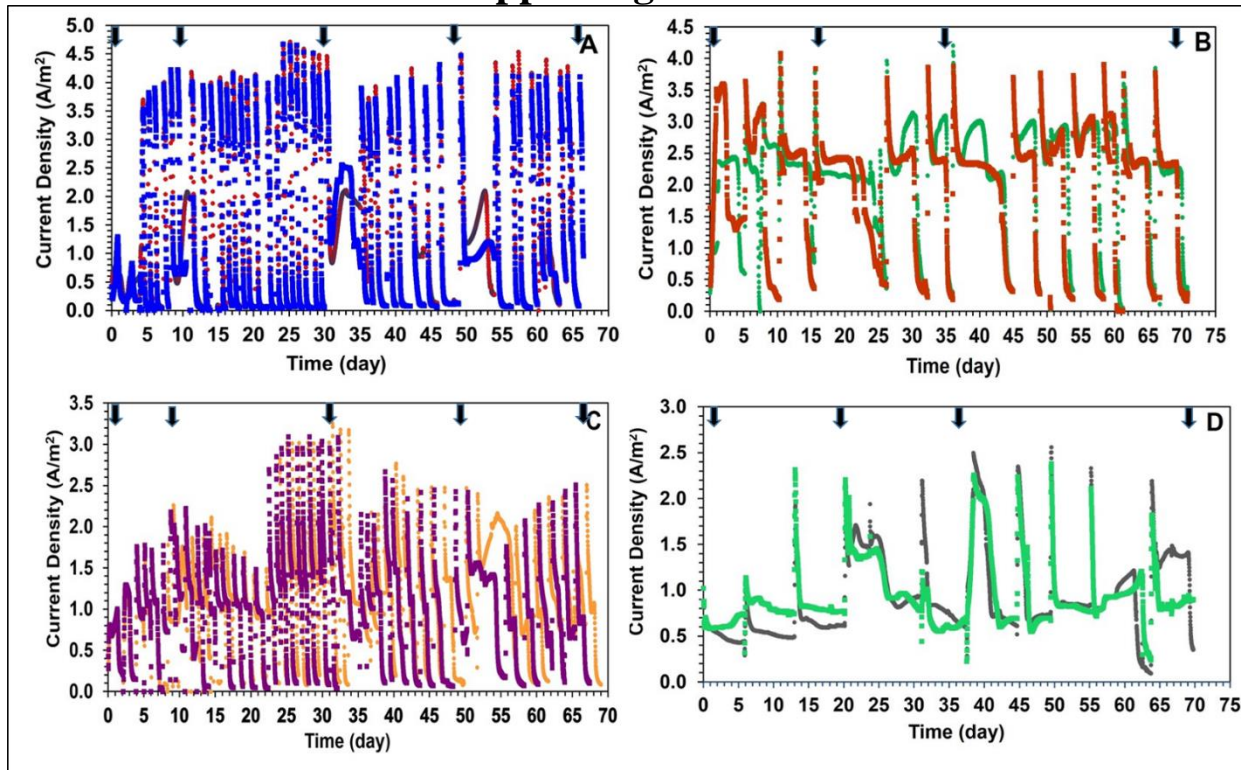
Taxa level (class)	Taxa level (order, family or genus)	S (PL-0)	S (PL-10)	S (PL-30)	S (PL-50)	S (PL-70)	S (PH-0)	S (PH-20)	S (PH-35)	S (PH-70)
<i>Deltaproteobacteria</i>	<i>Geobacter</i>	0.0	44.19±4.7	10.13±3.3	9.59±2.6	2.62±1	3.28±1.5	2.61±1.4	6.63±2.5	12.88±3.5
	<i>Desulfovibrio</i>	0.0	6.44±2.9	3.31±1.9	6.77±2.9	8.43±2.7	1±0.4	3.30±1.3	0.9±0.2	0.4±0.2
	<i>Desulfuromonadales</i>	0.0	1.38±0.9	0.5±0.3	0.0	0.0	0.3±0.1	0.3±0.1	0.3±0.1	2.77±1.4
	<i>Pelobacteraceae</i>	0.0	0.0	2.45±0.9	0.0	0.0	0.6±0.4	0.4±0.2	0.3±0.1	0.2±0.1
<i>Clostridia</i>	<i>Coprothermobacter</i>	19.28±2.7	0.5±0.3	1.33±1	0.4±0.2	0.3±0.1	17.70±4.4	4.54±2.1	1.63±0.7	0.4±0.2
	<i>Sedimentibacter</i>	0.7±0.2	10.26±3.3	2.86±1.2	3.58±1.6	1.96±0.7	0.5±0.4	14.14±4.3	7.65±2.6	7.53±2.2
	<i>Soehngenia</i>	8.98±2.1	0.0	0.0	0.0	0.0	6.44±2.6	1±0.4	0.4±0.1	0.3±0.1
	<i>Clostridiales</i>	0.9±0.6	7.87±2.6	0.7±0.3	3.6±0.9	0.6±0.2	0.5±0.2	2.49±1.6	3.6±1.1	4.6±1.9
	<i>Desulfosporomusa</i>	0.0	0.0	0.0	3.36±1.7	3.84±1.5	0.2±0.1	0.0	0.9±0.4	0.0
	<i>Syntrophomonas</i>	0.0	0.0	0.0	0.0	0.0	0.4±0.2	0.0	1.83±0.8	0.0
<i>Synergistia</i>	<i>Dethiosulfovibrionaceae</i>	11.30±2.8	2.93±1.4	1.84±0.7	11.56±3.1	11.90±2.8	16.7±5.1	2.80±1.2	29.68±3.9	5.52±2.3
	<i>Synergistaceae</i>	8.79±3.2	0.6±0.5	1.01±0.6	0.3±0.1	12.08±3.7	13.9±3.7	1.80±0.8	13.62±3.1	8.91±3.9
<i>Betaproteobacteria</i>	<i>Betaproteobacteria</i>	2.52±1.4	0.5±0.3	3.33±1.3	1.32±0.5	0.7±0.5	0.3±0.1	1.93±0.7	0.3±0.1	0.0
	<i>Rhodocyclaceae</i>	0.5±0.3	0.0	1.04±0.4	0.7±0.5	0.5±0.3	0.7±0.3	1.74±0.5	0.0	0.0
	<i>Thauera</i>	0.0	0.0	0.0	0.5±0.2	0.6±0.4	0.5±0.2	0.3±0.1	0.0	0.0
	<i>Dechloromonas</i>	0.8±0.5	6.06±3.7	41.32±6.3	18.51±4.5	2.15±1.7	1.49±1.1	37.45±5.2	3.36±1.2	5.80±2.7
<i>Gammaproteobacteria</i>	<i>Pseudomonadaceae</i>	0.6±0.4	2.96±1.1	12.19±3.2	4.70±2.2	1.21±0.4	12.5±3.5	5.7±2.5	0.5±0.2	0.4±0.2
	<i>Shewanella</i>	0.5±0.2	0.0	9.45±3.9	0.4±0.3	28.95±5.7	0.6±0.3	0.5±0.2	0.9±0.8	0.5±0.4
<i>Anaerolineae</i>	<i>Anaerolineae</i>	8.73±2.7	0.6±0.4	0.7±0.3	1.01±0.8	10.49±3.5	7.04±2.1	0.7±0.4	2.04±1.4	5.81±2.2
<i>Bacteroidia</i>	<i>Porphyromonadaceae</i>	2.39±1.4	1.49±0.6	1.1±0.4	7.11±2.8	2.06±1.6	3.08±1.5	3.5±1.8	1.52±0.4	19.23±4.1
	<i>Bacteroidales</i>	2.24±1.6	4.87±1.8	1.6±0.9	3.93±2.5	0.7±0.5	3.49±2.8	0.6±0.5	2.44±0.9	0.0
	<i>Dysgonomonas</i>	0.7±0.5	4.39±2.2	0.8±0.7	0.6±0.5	0.0	1.4±0.8	0.5±0.2	0.3±0.3	0.0
<i>Alphaproteobacteria</i>	<i>Telmatospirillum</i>	0.0	0.0	0.3±0.1	0.2±0.1	0.0	0.0	0.0	0.3±0.1	4.80±2.4
Others		31±4.2	5±2.4	4±1.4	22±4.8	11±3.5	7±2.6	14±3.1	21±3.9	20±2.7

Supporting Information



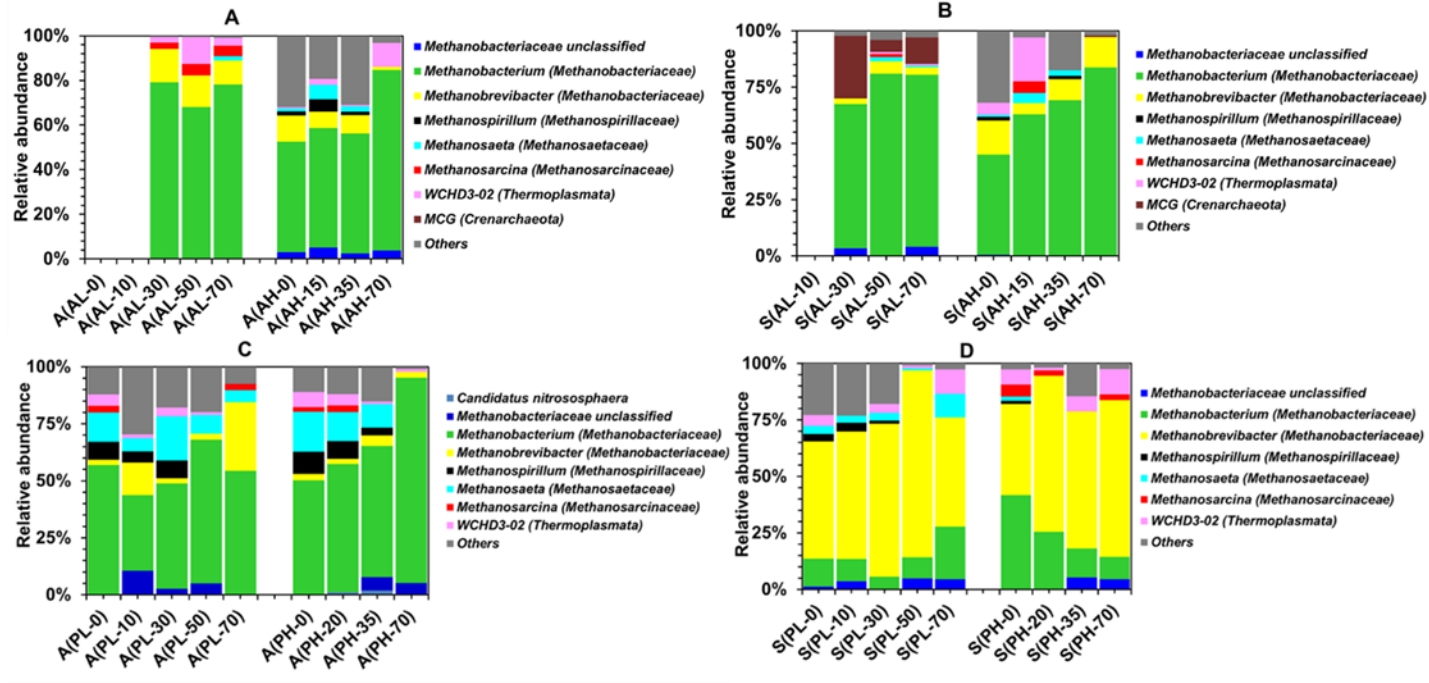
Supplementary Figure S1. Photo of the brush anode used in this study. The dashed rectangle represents the section of the anode that was sampled for microbial analysis.

Supporting Information



Supplementary Figure S2. Current density profile in duplicate MECs fed with low and high concentrations of acetate and propionate. (A) MECs fed with low acetate concentration (AL); (B) MECs fed with high acetate concentration (AH); (C) MECs fed with low propionate concentration (PL); (D) MECs fed with high propionate concentration (PH). Arrows indicate anode biofilm sampling for DNA extraction.

Supporting Information



Supplementary Figure S3. Relative abundance of archaeal phylotypes to the lowest classification level possible (class, family and genus) for the anode of A-reactors (A), suspension of A-reactors (B), anode of P-reactors (C) and suspension of P-reactors (D). A, anode and S, suspension. Archaeal phylotypes representing less than 1% of the relative abundance are classified as others. The taxa level shown on the right-hand side of the panel represents class, family and genus. Samples A (AL-0 and 10) and S (AL-0 and 10) failed to amplify.