Submission to Energy & Environmental Science

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Supplementary Information

Simultaneous organic carbon, nutrients removal and energy production in a photomicrobial fuel cell (PFC)

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The following is included as additional supporting materials for this paper:

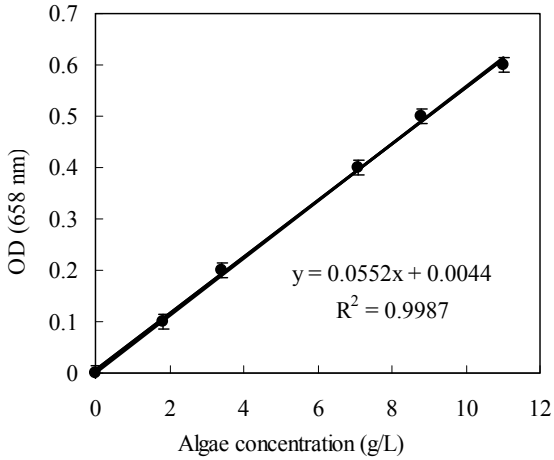

Figure S1. Algae concentration versus optical density (OD) at 658 nm (*C. vulgaris*) in synthetic wastewater.

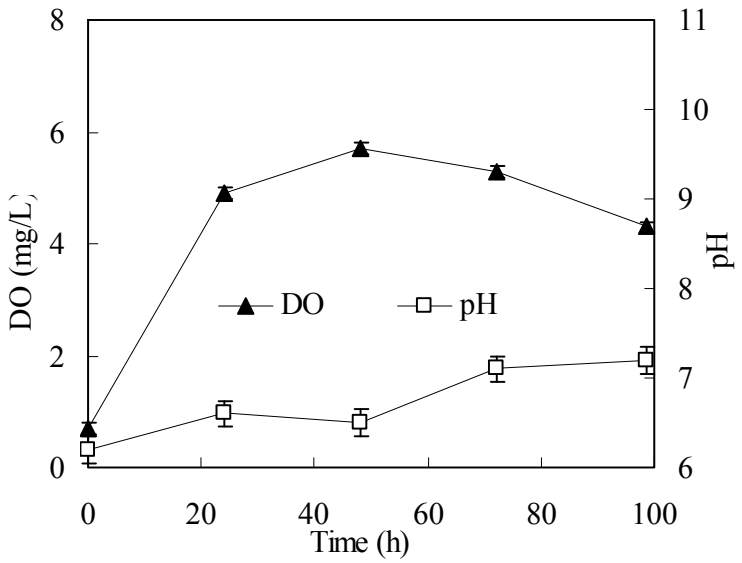

Figure S2. DO and pH change with time

Table S1. Sediment characteristics of Bagsvaerd Lake

Characteristics	Measured values
pH	6.5±0.1
Conductivity	495±10 ms/cm
Water content	25.0±0.2%
Organic content	17.5±0.3%
Total nitrogen	0.030±0.002 mg/g
Total phosphorus	0.011±0.001 mg/g

Table S2. DGGE 16S rDNA band identifications

Band	Sampling site[a]				Genbank accession no.	Closest relatives (%Sequence similarity[d])	Class[c]
	A	B	C	D			
1				•[b]	JF979184	Uncultured bacterium oca1 (96%)	*Alphaproteobacteria*
2	•	•	•		JF979185	Bacterium PE03-7G27 (99%)	*Gammaproteobacteria*
3	•	•	•	•	JF979186	Uncultured bacterium 4D3-5 (98%)	*Alphaproteobacteria*
4	•	•	•	•	JF979187	*Bradyrhizobium japonicum* 2M (99%)	*Alphaproteobacteria*
5	•	•			JF979188	Uncultured *Flavobacterium* sp. clone OHW4 (99%)	*Flavobacteria*
6	•				JF979189	Uncultured bacterium clone CJRA42 (95%)	*Flavobacteria*
7			•		JF979190	*Terrimonas ferruginea* CL-9.09b (98%)	*Sphingobacteria*
8		•	•		JF979191	Uncultured *Rhodoferax* sp. FL_51 (98%)	*Betaproteobacteria*
9	•	•	•	•	JF979192	Uncultured bacterium R3B-14 (97%)	*Flavobacteria*
10	•	•		•	JF979193	Uncultured bacterium clone BACd-6E3 (100%)	*Sphingobacteria*
11		•		•	JF979194	*Rhizobium* sp. AL9.3 (99%)	*Alphaproteobacteria*
12	•	•	•	•	JF979195	Denitrifying bacterium W73c (100%)	*Alphaproteobacteria*
13	•			•	JF979196	Uncultured bacterium MIZ33 (99%)	*Alphaproteobacteria*
14				•	JF979197	*Alpha proteobacterium* D8-16 (99%)	*Alphaproteobacteria*
15	•	•	•		JF979188	Uncultured *Flavobacterium* sp. clone OHW4 (99%)	*Flavobacteria*

[a] Sampling sites as shown in Figure S2.
[b] Existence under the condition
[c] The phylotypes were assigned to phyla based on Ribosomal Database Project II (RDP II) taxonomy classifications
[d] Percent values represent similarities between the associated DGGE band sequence and the closest match sequence from GenBank.