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SUPPLEMENTARY INFORMATION
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Electroactive microorganisms in bioelectrochemical systems

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Supplementary Box 1. Methods for Figure 2.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Jukes-Cantor model [1]. The tree with the highest log likelihood (-23697.65) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. Bootstrap support values (≥70%) are given, based on 1000 tree iterations. The analysis involved 62 nucleotide sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 1242 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2]. Sequences were retrieved from the NCBI database and aligned with MUSCLE [3] using the Neighbor-Joining clustering method, with -400 gap open penalty and a maximum of 8 iterations.

The methods for Figure 2B are the same as those for 2A, except as noted. The tree with the highest log likelihood (-18306.95) is shown. The analysis involved 39 nucleotide sequences. There were a total of 1177 positions in the final dataset.

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Supplementary Box 2. Microorganisms in Figure 3.

The red color indicates yeast extract was used in the medium.

Notation: 2CA= Two chamber MFC; 1CA=1 chamber MFC.

Acetobacter aceti[1]
Arcobacter butzleri[2]
Bacillus subtilis[3,4]
Clostridium butyricum[5]
Corynebacterium strain MFC03[6]
Enterobacter aerogenes[7]
Enterobacter cloacae[8]
Enterobacter cloacae[9]
Escherichia coli W3110[10]
Escherichia coli BL21[11]
Escherichia coli DH5α[12]
Geobacter sulfurreducens PCA[13]
Geobacter sulfurreducens PCA[14]
Geobacter sulfurreducens KN400[15]
Gluconobacter roseus[1]
Klebsiella pneumoniae[16]

Lysinibacillus sphaericus D-8[17]
Lysinibacillus sphaericus VA5[18]
Ochrobactrum anthropi[19]
Proteus vulgaris[20]
Pseudomonas aeruginosa KRP1[21]
Pseudomonas aeruginosa[22]
Rhodoferax ferrireducens[23]
Rhodopseudomonas palustris DX1[24]
Shewanella oneindensis MR-1[25]
Shewanella oneindensis MR-1[26]
Shewanella putrefacians[27]
Tolumonas osonensis[28]
Candida melibiosica[29]
Saccharomyces cerevisae[30]
Haloferax volcanii[31]
Natrialba magadii[31]
Pyrococcus furiosus[32]
Mixed culture (2CA)[33]
Mixed culture (1CA)[34]
Mixed culture (1CA)[35]

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Supplementary Box 3. Microorganisms in Figure 4.
The red color indicates yeast extract was used in the medium.

Sporomusa ovata [DSM-2662][1]
Sporomusa ovata [DSM-2663][2]
Sporomusa ovata [DSM-3300][2]
Sporomusa acidovorans [DSM-3132][2]
Sporomusa malonica [DSM-5090][2]
Sporomusa aerivorans [DSM-13326][2]
Rhodopseudomonas palustris [TIE-1][3]
Clostridium ljungdahlii [DSM 13528][4]
Clostridium pasteurianum [DSM-525][5]
Cupriavidus necator [DSM-13513][5]
Cupriavidus metallidurans [DSM-2839][5]
Acidithiobacillus thiooxidans [DSM-14887][5]
Acidithiobacillus ferrooxidans [DSM-14882][5]
Thiobacillus denitrificans [DSM-12475][5]
Sulfurimonas denitrificans [DSM-1251][5]
Desulfosporosinus orientis [DSM-765][5]
Desulfovibrio piger [DSM-749][5]
Methanobacterium palustre [ATCC BAA-1077][6]
Methanothermobacter thermautotrophicus ΔH[7]
Methanococcus maripaludis MM901[8]
Methanobacterium IM[9]

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